

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: March 2, 2005, 06:00:31 : Search time 3385 Seconds
(without alignments)
9175.907 Million cell updates/sec

Title: US-10-720-018-1
perfect score: 816
Sequence: 1 atggatgactacatccaac.....atggatgtttcaactcttgg 816

Scoring table:

IDENTITY-NUC

Gapop 10.0 , Gapexit 1.0

Searched: 34239544 seqb, 19032134700 residues

Total number of hits satisfying chosen parameters:

68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

'EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gb81:*

9: gb_gb82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

LOCUS

DEFINITION

T7 end of clone BB0AA014611 library BB0AA from strain CBS 4732

of *Pichia angusta*, genomic survey sequence.

GSS.

AL433186.1 G1:12216600

KEYWORDS

GSS.

ORGANISM

Pichia angusta

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetidae; *Saccharomycetaceae*; *Pichia*.

REFERENCE

1 (bases 1 to 899)

AUTHORS

Souciet,J.L., Aigle,M., Artigueneau,F., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durren,P., Lepingle,A.,

Malpertuy,A., Neuvraille,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekla,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEMS Lett. 487 (1), 3-12 (2000)

JOURNAL

MEDLINE

2058471

2058471

11152876

11152876

2 (bases 1 to 899)

the other extremity of this insert.

FEATURES source

Location/Qualifiers

1. .-899

/organism="Pichia angusta"

/mol_type="genomic DNA"

/db_xref="taxon:4905"

/clone="B00A_014G11"

/clone_id="B00A"

/note="end : T7"

<18 . .>633 <18 . .>633

/note="similar to P50167 [d-arabinitol 2-dehydrogenase ARDH] [Pichia stipitis]

1 putative frameshift (8)

/evidence-not_experimental complement(<729 .->812)

/note="similar to *Saccharomyces cerevisiae* ORP YKL126w [YPK1 ; serthr-specific protein kinase]"

/evidence-not_experimental complement(<732 .->812)

/note="similar to *Saccharomyces cerevisiae* ORF YMR104c [YPK2 ; serthr_protein_kinase]"

/evidence-not_experimental

ORIGIN

Query Match

33.9%; Score 276.6; DB 9; Length 899;

Best Local Similarity

66.0%; Pred. No. 3.6e-68;

Matches

416; Conservative

0; Mismatches

210; Indels

4; Gaps

1;

Matches

416; Conservative

0; Mismatches

210; Indels

4; Gaps

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Matches

416; Conservative

0; Mismatches

210; Indels

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Matches

416; Conservative

0; Mismatches

210; Indels

4; Gaps

1;

Matches

416; Conservative

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210; Indels

4; Gaps

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210; Indels

4; Gaps

1;

Qy	664	GATTGTCACAGATGATCTGGTATCCACACAAGATGTCGAGCAAGGAA 723	134	ACCGAGAAAAGACTGCTGCCAACAAAGCCGATAACCAAA 190	Qy
Db	610	GATCTAAGGCCAATGGCAGACTTCCTTATCCCGAGGCAAATGGCAC 669	140	ATAAGGAAGAAAGAGAGAGAGGAGGAACTGTTGATCATGGAGAGAAC 199	Db
Qy	724	TACATTGGCTGTGTTGACTTGCTTCTGAATCTGCCTCATACACTACTG 783	191	TGAGTTGAAGAGAGTCCAAGATGGGTCTATGCCCTGATATTCTGATCTGATA 250	Qy
Db	670	CTCATGGGCCCTGGCATTCYCCATCAGA---TCTCTCTGATGTACTGGGCC 726	200	CTCAGGCCAGATACTCCAAAGTCAGCTGCCATTATGCTGATGTTCTKATCTGAT 259	Db
Qy	784	AGCTTACTGTTGATGGTGTTCAC 809	251	CGITCACAGGTGTTGCTCAACTGCTAAGGATTGGTAAGTGGCAATTGACTGG 310	Qy
Db	727	CACATCGAATCTCATGGGGCTAC 752	260	CTGAGGCTGTAGCGAGGTGTTAGGAGCAGGAAGATGACA---ACCTGG 316	Db
Qy	RESULTS 3		311	TAACACAGCTGGTACTCTGAAACTCCCACTGTGAAGATTAACCAAGGAC 370	Qy
LOCUS	BT750180	BT750180 682 bp mRNA linear EST 14-JUN-2004	317	TACCTCACCTGGCTTACGGAGACTCTGAAAGATTAACCAAGGAC 370	Db
DEFINITION		Fg02_10b03_R Fg02_AAFC_ECORI Gibberella zae cDNA clone Fg02_10b03, mRNA sequence.	371	AGAGATGGTGAAGTTACTCTGGTTCTGTGATGTTCTCAAGCTCTCTAAC 430	Qy
REFERENCE		Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. [bases 1 to 682]	377	GTAGCTTGGCTTAACTGTTGACGSGTACATATYCTTGTGACATCTAGTGCCAGY 436	Db
AUTHORS		Harris, L.J., Glasco, T., Rochefeuille, H., Allard, S., Chabados, J., Courteau, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D., and Tinker, N.A.	431	CATGAT-CAAGAGGATTCACAGGGTGTCTGTGTTGATGGTCTCTGTT 489	Qy
VERSION		Expressed Sequence Tags from Fusarium graminearum mycelium Unpublished (2001)	437	ACTTATGCGAAAGAAGSTCTCGTAGATC---GCTATGTTGAGCTACGTCGGA 492	Db
KEYWORDS		Contact: Harris, Linda J. Eastern Cereal and Oilseed Research Centre Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA	490	GCTATGGTCAAGATCTCAAACCAAGTGTACACATGTCGAAGCTGGTTAAC 549	Qy
JOURNAL		Tel: (613) 759-1314 Fax: (613) 759-6566 Email: harrisj@agr.gc.ca.	493	TCTATGTCACAGTCTCTAGGCTTACGGCTCTCTATAGTGCYCCAAAGCYGGTGC 552	Db
COMMENT		1. .682 /organism="Gibberella zae" /mol_type="mRNA" /strain="DAOM 180378" /db_xref="taxon:5518" /clone="Fg02_10b03" /tissue_type="Mycelial tissue" /dev_stage="Asexual" /lab_host="E. coli (sure cells)" /clone_id="Fg02_AAFC_ECORI_Fusarium_graminearum_mycelium" /note="Vector: Bluescript SK+/XbaI-BcORI; Site 1: BcORI; site 2: XbaI; Mycelial tissue was collected from V8 agar plates after a growth period of 6-7 days at 25 C with 14 hrs (FL/UV) day light exposure. Mycelia was ground in liquid nitrogen prior it's storage at -80 C until RNA extraction. Directional cloning with 5' end of DNA cloned into BcORI site of plasmid and 3' end of cDNA cloned into XbaI site of pBluescript (Stratagene, La Jolla, CA)."	553	CATGGCTAAAGCTTGCTGTGATGGTCTAAGTACACATCAGTTAATCTTA 609	Qy
FEATURES	source	1. Location/Qualifiers	610	ACCCAGGTACATCTACGGCTCTTGACCAAGAAGATTTATATGGTACCGA 665	Db
FEATURES	source	1. Location/Qualifiers	613	TCTCGGGTACATGTTGACTGACTCTACATCAGAGAAATCTGCGACACCGGA 668	Db
RESULTS 4					
LOCUS	CF677471/c	CF677471 713 bp mRNA linear EST 16-AUG-2004			
DEFINITION		CCAT90TF C.neoformans strain JE21 Cryptococcus neoformans var. neoformans cDNA clone CCI990, mRNA sequence.			
REFERENCE		CF677471			
VERSION		CF677471.1			
KEYWORDS		EST.			
SOURCE		Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)			
ORGANISM		Cryptococcus neoformans var. neoformans Bukaryota; Fungi; Basidiomycota; Zygomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella			
REFERENCE		I (bases 1 to 713)			
AUTHORS		Lofthus, B.			
TITLE		Brd sequencing of clones from a full length enriched, normalized JE21 cDNA library			
JOURNAL		Unpublished (2003)			
COMMENT		Other ESTs: CCI990TR Contact: Brendan Loftus			
ORIGIN		TIGR Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5543 Fax: 301-838-0208 Email: crypt@tigr.org			
Query Match		14.5%; Score 118.4; DB 4; Length 682;			
Best Local Similarity		52.1%; Pred. No. 1.2e-22;			
Matches	342;	Conservative 8; Mismatches 295; Indels 11; Gaps 4;			
Qy	14	TTCACACTTGTGATCGATGCCACTTAACTTGTGACACTGCTCCCTGGGGTTAG 73	1. .713 /organism="Cryptococcus neoformans var. neoformans"		
Db	20	TGCCACCTTACACTCGACGGTCATGTTGCGATCTGGACAGCTGCTGATATCG 79	/mol_type="mRNA" /strain="JEC21" /db_xref="taxon:40410" /clone="CC1990"		
Qy	74	CTGAGCTTAATCAGGGTTGGCTACGGTCTGACATGCTGCTGATATCG 133			
Db	80	GCTGGTGTATGGCTCAAGAATGATCTCTGATCCAACTCTGCTGATATW 139			

/note="Vector: pCMVSPORT6; Site_1: NotI-EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Jennifer Lodge"

ORIGIN

Query Match 13.9%; Score 113.4; DB 7; Length 713;
Best Local Similarity 54.6%; Pred. No. 3.5e-21;
Matches 278; Conservative 0; Mismatches 216; Indels 15; Gaps 2;

Qy 308 TGGTTAACACAGCTGGTACTGTGAAACTTCCATGTGAGATGCCAACCAAGC 367
Db 649 TGGTCACTGCTGCCGTTATTGCGAAACTTGTCGTCAGAGTACCCCTTGATAA 590

Qy 368 CTGAGAAGATGGGAAGGTATCAAGGGTCTGTTGTTGATGTTCTAACCCTTGCA 427
Db 589 TCAAGAAGACTGTGGACATCACATTAATGGTACTGTTATGGCACTTGGCTGCA 530

Qy 428 AGCCATGATGCTAACGATCTCTCAAACCAAGTGTCTACAAGATGTCAGGCTGGTAA 487
Db 529 AGCTTATGCCCTGA-----GGTGTTCATTAACCTCGTGCATATGAGCG 482

Qy 488 GTCATCATGTCAGCATCTCTCAAACCAAGTGTCTACAAGATGTCAGGCTGGTAA 547
Db 481 GPGACATGTCACGTTCTAACCTCAAACCCCTTACAATTTCAASGCTGCTGTC 422

Qy 548 TCCATTGGCTAAAGCTTGGCTGTGAAATGGCTAAAGTACACATCAGAGTTAATCTT 607
Db 421 GACACATGCTCATCCCTGCCGTCGAATGGCTCTCAAGGTTACCGTCAAGGCTC 362

Qy 608 TAACCCAGGTACATCTACGTTGCTGAAAGAAGATGTTATCAATGGTACAGGAAT 667
Db 361 TTAGTCGGGTATGCTCCTACCAACTTGACTAAGGTCTGACGCCACCGTTC 302

Qy 668 TGTACACAGTAGTGTCTGTTGTTATCCACACAAAGATTCGGACAAAGGAATACA 727
Db 301 TCGTGACGAGGAGGTCAACGTTACCTGCTTGCTGAAATGGCTTCTGTGATCTA 242

Qy 728 TGGTGTGTGTTGTTGACTGTGTTCTGAACTGTGCTGTTCTACACTACTGTTGGCAAGCT 787
Db 241 AGGGTGCCTCATTTACTTGCTCTGA---CAGCTCAAGTACACCACTGTGCTGAGA 185

Qy 788 TACTGGTGTGATGGTGTCTCTGG 816
Db 184 TCATGATGACGGGGTACACTTGCTG 156

Email: crypt@tigr.org
Seq primer: TF.
FEATURES
Source

1. .835
/organism="Cryptococcus neoformans var. neoformans"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CACTr16"
/note="Vector: pCMVSPORT6; Site_1: NotI-EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 13.9%; Score 113.4; DB 7; Length 836;
Best Local Similarity 54.6%; Pred. No. 3.7e-21;
Matches 278; Conservative 0; Mismatches 216; Indels 15; Gaps 2;

Qy 308 TGTTAACACAGCTGGTACTGTGAAACTTCCATGTGAGATGCCAACCAAGC 367
Db 665 TGGTCACTGCTGCCGTTATGTCGAAACTTGTGCTCACAGTACCCATCGATAA 606

Qy 428 AGCCATGATGCTAACGATCTCTCAAACCAAGTGTCTACAAGATGTCAGGCTGGTAA 487
Db 368 CTGAGAAGATGGGAAGGTATCAAGGGTCTGTTGATGTTCTGATGTTCTAACGCTTGTA 427

Qy 605 TCAAGAAGCTTGGACATCACATTAATGGTACTGTGTTATGGCTATGGCACTTGAGGCTGCA 546

Qy 488 GTCATCATGTCAGCATCTCTCAAACCAAGTGTCTACAAGATGTCAGGCTGGTAA 547
Db 545 AGCTTATGCTGAA-----GGTGTTCATTAACCTGCTGCTGCTGTC 498

Qy 488 GTGCCATGTCACGATCCCTCAAACCAACTGTGTTCTACACATGTCACAGGCTGTGTA 547
Db 497 GTAGCATGTCACGTTCTAACCTCAAACCCCTAACCTTCAAAGGCTCTGTGTC 438

Qy 548 TCCATTGGCTAAGACTTGCTGTTGANTGGCTAAGTCAACATCAGTAACTCTGTC 607
Db 437 GACACATGGCTGATCCTGCCGCTGAAATGGCTCTAACGGTATCCGTCAACGTC 378

Qy 608 TAACCCAGGTACATCTACGTTGCTGTTGACCAAGAATGTTATCAATGGTAACGAGAAT 667
Db 377 TTAGTCGGGTATCCTCTACCAACTTGACTAAGGTCTCTCGACGCCAACCGTTC 318

Qy 668 TGTACACAGTAGTGTCTGTTGATCCACACAAAGATGTCGCCAACCAAGGAATACA 727
Db 317 TCGTGACGAGGAGGTCAACGTTACCTGCTGTTGACCAAGAATGTTATCAATGGTAACGAGAAT 258

Qy 728 TTGGTGTGTGTTGACTTGCTTGAACTGTGCTGCTCATACTACTGTTGGCTGAGCT 787
Db 257 AGGGTGCCTCATTTACTTGCTCTGACGCTCCAA---TACACCCTGGTGTGAGA 201

Qy 788 TACTGGTGTGATGGTGTCTCTGG 816
Db 200 TCATGATGACGGGGTACACTTGCTG 172

RESULT 6
LOCUS CFT15948/c
DEFINITION CFT15948 mRNA linear EST 16-AUG-2004
ORGANISM Cryptococcus neoformans var. neoformans
REFERENCE 1 (bases 1 to 836)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a full length enriched, normalized JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CACTr16
Contact: Brendan Loftus
TIGR Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Pax: 301-838-0208

RESULT 5
LOCUS CFT01403
DEFINITION 835 bp mRNA linear EST 16-AUG-2004
ACCESSION CFT01403
VERSION CFT01403.1
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM Eukarya; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
REFERENCE 1 (bases 1 to 836)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a full length enriched, normalized JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CACTr16
Contact: Brendan Loftus
TIGR Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Pax: 301-838-0208

RESULT 6
LOCUS CFT15948
DEFINITION CFT15948 mRNA 836 bp mRNA linear EST 16-AUG-2004
ACCESSION CFT15948
VERSION CFT15948.1
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukarya; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
REFERENCE 1 (bases 1 to 836)

Db	234	GATTGAGGGTATGGGGTACACTT	207	Qy	664	GAATTCTACACAGATGGATCTCGTATCCACACAGATCTCGAACCAANGA	723
RESULT	8			Db	349	GATCTCAAAGAAAGTGACCTCCCTCATTCACAGCAATTGGTACACCTGAGAC	290
CF82542/c				Qy	724	TACATGGTGTGTTGACTTGCTCTGATCTGCTGCTCTCATACACTGGGCC	783
LOCUS	CPR34542	787 bp	mRNA	DEFINITION	EST01924 Coccidioides posadasii saprobic phase cDNA library, 2 to	EST 01-APR-2004	
DEFINITION				4	bases 1 to 787)	4 kb Coccidioides posadasii cDNA clone CIDAR90 3' end, mRNA	
SEQUENCE				REFERENCE	Gardner,M.J. and Cole,G.T.		
ACCESSION	CF82542			AUTHORS			
VERSION	CF82542.1			TITLE			
KEYWORDS	EST.			JOURNAL			
SOURCE	Coccidioides posadasii			COMMENT			
ORGANISM	Coccidioides posadasii			Contact:	Gardner MJ		
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				Other_ESTs:	EST701925		
Oryginales; mitosporic Onygenales; Coccidioides.				The Institute for Genomic Research			
1 (bases 1 to 787)				9712 Medical Center Drive, Rockville, MD 20850, USA			
Authors	Gardner,M.J. and Cole,G.T.			Tel:	301 838 3519		
TITLE				Fax:	301 838 0208		
JOURNAL				Email:	gardner@tigr.org		
COMMENT				Features			
CONTACT				source			
Other_ESTs:	EST701925			Location/Qualifiers			
Other_ESTs:	EST168965			1. -787			
Contact:	Gardner MJ			/organism="Coccidioides posadasii"			
The Institute for Genomic Research				/mol_type="mRNA"			
9712 Medical Center Drive, Rockville, MD 20850, USA				/strain="C735"			
Tel:	301 838 3519			/db_xref="taxon:199306"			
Fax:	301 838 0208			/clone="CIDAR90"			
Email:	gardner@tigr.org			/dev_stage="saprobic phase (mycelia)"			
Features				/lab_host="E. coli DH10B, T1 phage resistant"			
source				/clone_lib="Coccidioides posadasii saprobic phase cDNA			
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ORIGIN				COMMENT			
Query Match	13.8%	Score 112.B; DB 7; Length 787;		CONTACT			
Best Local Similarity	54.1%	Pred. No. 5.3e-11;		Other_ESTs:	EST168965		
Matches	275;	Conservative 0; Mismatches 227;		Contact:	Gardner MJ		
Db	706	Indels 6; Gaps 2;		The Institute for Genomic Research			
Qy	304	CACTGGTTACACAGCTGTACTCTGAAACTCCATCTGAGATTAACCGCAAG	363	9712 Medical Center Drive, Rockville, MD 20850, USA			
Db	706	/clone=CATCTGGTCACATCTGGGGGTACTGAAACTCTGAGCTGCTACCCGATG	647	Tel:	301 838 3519		
Qy	364	AACTCTGAGAGATGGTGAAGGTTAACTGTGTTGCTTGTGATGTTCTCAAGCTT	423	Fax:	301 838 0208		
Db	646	/clone=CIBA94"		Email:	gardner@tigr.org		
Qy	424	/dev_stage="saprobic phase (mycelia)"		Features			
Db	586	/lab_host="E. coli DH10B, T1 phage resistant"		source			
Qy	586	/clone_lib="Coccidioides posadasii saprobic phase cDNA		Location/Qualifiers			
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Qy	424	Coccidioides posadasii saprobic phase cDNA library, size		/organism="Coccidioides posadasii"			
Db	586	fractionated cDNA > 4 kb"		/mol_type="mRNA"			
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Db	435	fractionated cDNA 2 to 4 kb"		/strain="C735"			
Qy	664	/clone="CIBA94"		/clone="CIBA94"			
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Qy	364	/lab_host="E. coli DH10B, T1 phage resistant"		/lab_host="E. coli DH10B, T1 phage resistant"			
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Qy	424	/note="vector: pEXPRESS 1; Site_1: Not I; Site_2: Eco RV;		/note="vector: pEXPRESS 1; Site_1: Not I; Site_2: Eco RV;			
Db	492	Coccidioides posadasii saprobic phase cDNA library, size		/note="vector: pEXPRESS 1; Site_1: Not I; Site_2: Eco RV;			
Qy	484	fractionated cDNA 2 to 4 kb"		/note="vector: pEXPRESS 1; Site_1: Not I; Site_2: Eco RV;			
Db	436	/strain="C735"		/strain="C735"			

QY 544 GTTATCCATTGCTAAGACTTGGCTGGAATGGCTAACATACTAGAGTTAT 603
Db 375 ATAGGCACTTGCTCTTCGCACTTGATGGCAAGTGAACTAGAGTAC 316
QY 604 TCTTAACCAGGTAGATCAGGGCTTACCGAGAGTTACATGTTACAGAA 663
Db 315 TGTATCAGTCAGGATACATGTTGACTGCCCTGACCGCAACATTCTGAC 256
QY 664 GATGTAACAGAGATGGCTGATCCAAAGAGATGTCGACAAAGAA 723
Db 255 GATCTCAAGAGAGTGGCTGACCCCTTCAAGGCAAATGGTACACTGGAGAC 196
QY 724 TACATGGCTGCTTGTACTGCTTGATGTCCTGCTCATCACTACTGGGCC 783
Db 195 CTGATGGCCCACTGACCTTCTATTGAGTGA---TGCAGCAATATGTTACTGGGCA 139
QY 784 AGCTTACTGGTATGGGTTTCACT 811
Db 138 GATTGAGGGTGATGGCGGGTACATT 111

RESULT 10

LOCUS CF824543 676 bp mRNA linear EST 01-APR-2004
DEFINITION EST01925 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAK90 5', end, mRNA sequence.

ACCESSION CP824543
VERSION CF824543.1
SOURCE EST.
ORGANISM Coccidioides posadasii
Coccidioides posadasii
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.
AUTHORS Gardner,M.J. and Cole,G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
COMMENT Unpublished (2003)
Other ESTs: EST70124
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse
FEATURES source
1. . 676
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIDARR90"
/dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/codon_libraries="Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb"
/note="vector: pEXPRESS 1; Site_1: Not I; Site_2: Eco RV; Coccidioides posadasii saprobic phase cDNA library, size fractionated cDNA 2 to 4 kb"
ORIGIN

Query Match 13.0%; Score 106.4; DB 7; Length 676;
Best Local Similarity 58.6%; Pred. No. 3-6-19; Matches 204; Conservative 0; Mismatches 141; Indels 3; Gaps 1;

QY 464 TGTATCAGTCAGGATACATGTTGACTGCCCTGACCGCAACATTCTGAC 523
Db 121 TTGTGTCATGGAGACATGTCGCTGGCCATTAACTGGCTCAGGCCGCT 180
QY 524 ACGACATGTCAGGCTGGTATCCATTGGCTAACACTTGGCTGATGGCTA 583

RESULT 11

LOCUS AJ638396 718 bp mRNA linear EST 05-MAY-2004
DEFINITION AJ638396 Mgc Mycosphaerella graminicola cDNA clone mgc06e02f, mRNA sequence.

ACCESSION AJ638396
VERSION AJ638396.1
TITLE GI:47011453
KEYWORDS EST.
SOURCE
ORGANISM Mycosphaerella graminicola
Mycosphaerella graminicola
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Mycosphaerellaceae; Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; Mycosphaerella.
AUTHORS Keon,J.P.R., Hargreaves,J.A., Antoniw,J.F. and Hammond-Kosack,K.
TITLE Analysis of expressed sequence tags from the wheat fungal leaf blotch pathogen, Mycosphaerella graminicola (anamorph Septoria tritici)
JOURNAL Fungal Genet. Biol. (2004) In press
COMMENT Contact: Keon J
Plant Pathogen Interactions Division,
 Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44(0) 1582 765133
Fax: +44(0) 1582 760981
Email: John.keon@bbrc.ac.uk
Insert length: 800 Std Error: 100.00
Seq primer: M13 reverse
FEATURES source
1. . 718
/organism="Mycosphaerella graminicola"
/mol_type="mRNA"
/strain="Mgc"
/db_xref="taxon:54734"
/clone="mgc06e02f"
Query Match 12.6%; Score 102.8; DB 1; Length 718;
Best Local Similarity 53.0%; Pred. No. 46-18; Matches 268; Conservative 0; Mismatches 232; Indels 6; Gaps 2;
Matches 268; Conservative 0; Mismatches 232; Indels 6; Gaps 2;
QY 304 CACTGGTAAACACAGGTGTTACTGTGAAACTTCCATGTGAAAGTTACCGCCAG 363
Db 49 CACCTCTCACCTCCGCTGGCTCACGGAGACTGGACGCCATCGTACCCACAGGAC 108
QY 364 AACGCTGAGAGATGGTGAAGTTAACCTGTTGGTGTGTTGTGATGTTCTCAAGCTT 423
Db 109 CGATGCGAGAGCTTGGGAGTCAGTCAGGCCACATCTGCTCTGACCGCTG 168

424 GCTTACGACCATATCAGAAGCTTAAGGTGCTCTGTTGTTGATGGTTCATG 483
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 169 GCGAACT---ATCTCTGAGCGCAAGCTCTGGAGCTGTGAGTGTGACATG 225
 REFERENCE TCTGGTCCATATGTCACAGATCTCAAACCAAGTGTGCTACAGCTGAGTGGT 543
 AUTHORS 226 TCTGGGCCATCTGCACTGCTGCTGCTGAGCTGAGGTGGT 285
 TITLE 544 GTTATCCATTGCTAGACTTGGCTGATGCTGCTGAGCTACACATGAGTTAAT 603
 FEATURES Db 286 GTCGGCATCTGGCACTCGCTCGACTGAGCTGAGCTGAGCTACACATGAGTTAAT 345
 source QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 604 TCTTAAACCCGGTACATCTAGGCTCTTGACCGAAGTGTATCAAGTAGAA 663
 LOCUS 346 TGCATCTCTCCUGGCTACATGCTCACGCTCACGCTCACGAGATCCCTGAGCACACCCC 405
 DEFINITION QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 664 GATTTTACAACAGATGATGATCTCTGGTATCCACACAGAACAGATGTCGAACAAAGAA 723
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 406 GAGCTGCCAACAGTGGACCGCTATCCACAGGGCACAGTGGTGGCCAGAGAC 465
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 724 TACATCTGGCTTGTACTGTGTTCTGAATCTCTGCTCATACACTACTGGGCC 783
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 466 CTGAGGGCCGCTGACTTCTCTCAGCGA---GGCGGGATAGTGACGCCGCC 522
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 784 ACCTTATGGTATGGGGTTTCA 809
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 523 GATTCCTGGTGAACGGTGGATAAC 548
 ORIGIN

RESULT 12

CO136295 CO136295 615 bp mRNA linear EST 17-JUN-2004
 Locus EST83b966 Aspergillus flavus Normalized cDNA Expression Library
 Definition Aspergillus flavus cDNA clone NAFFQ16 5' end similar to D-arabinitol 2-dehydrogenase [ribulose forming] (EC 1.1.1.250)
 (ADPH). [Yeast] {Candida tropicalis}, mRNA sequence.

ACCESSION CO136295
 VERSION CO136295.1
 KEYWORDS GI:48885273
 SOURCE EST.
 ORGANISM Aspergillus flavus

REFERENCE
 AUTHORS Yu.J., Whitelaw,C.A., Nierman,W.C., Bhatnagar,D. and Cleveland,T.E.
 TITLE Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops
 JOURNAL FEMS Microbiol. Lett. (2004) In press
 COMMENT Contact: Yu J
 Food and Feed Safety Research Unit
 USDA/ARS, Southern Regional Research Center
 1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
 Tel: 504 286 4405
 Fax: 504 286 4419
 Email: Jiuyu@rrrc.ars.usda.gov
 Contact Dr. Yu at USDA/ARS SRRC (jiuyu@rrrc.ars.usda.gov) for clone information
 PCR PRIMERS
 FORWARD: M13R
 BACKWARD: M13F
 POLY-A=No
 FEATURES
 source Location/Qualifier^b
 1. . 615 /organism="Aspergillus flavus"
 /mo_type="mRNA"
 /strain="NRRRL 3357"
 /db_xref="txon:5059"
 /clone="NARFBQ16"
 /sex="asexual mycelia"
 /cell_type="mycelia"
 /dev_stage="developmental stages from 18 to 96 hours"

Query Match 12.4% Score 100.8 DB 7; Length 615;
 Best Local Similarity 51.2%; Pred. No. 1; e-17; Indels 6; Gaps 2;
 Matches 287; Conservative 0; Mismatches 267;

Db 196 TCTAAAGAGTCTCAAGATGGCTCTATGCTGTGATATTCCTGATTCATACCGTT 255
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 38 TCGAACAAATGCCACAGTCACGCCACTACGGCTAGCTGCTAGTTCGACCTACTCCGTC 97
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 256 CTCAGGGTTGCTCAAGTCTCTAAGGTTGGTAGTGTAGTCATGCACTGGTAAAC 315
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 98 AACGATSCCTCTCGATATTATCTCCAGCAAGCAGGAT---CGACAACCTGGTAC 154
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 316 AACGCTTATGTAACCTCCATGAGATACCCACGAGACCTGAGAG 375
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 155 TCGGCGATTCAGGAAACTCTGATGCCATCTCCATACCCCTACGACCTGTGCAAAG 214
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 376 ATGGTGAGGTTACTGTGGTCTTGTGTTCTCAAGCTGAGAG 435
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 215 CTGGGGGGTAACTGATGAGAACATACCTTCTCCACCGGTGGTGCACG--AC 271
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 436 ATCAAGAGGGTAACTGGGCTCTCTGTTGTTGATGGTCTCTGCTGTGCATT 495
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 272 CTCTGGAGGCGAGGTCTCGGGCAGCATGTCATGATGGTACGATGCTGTGCTAC 331
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 496 GTCACAGATCTCAACCAAGTGTACACATGTCACAGCTGCTGTTCTCAAGCCCTGCTAGCCATG 555
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 332 GTCACAGTGGCCAGGCCAGCTCTTACAGGCCAACGGCGCTGTTGCAACT 391
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 556 GCTAACAGTTGGCTGTGAAATGGGCTAACTCACATCAGGTTAACTCTAAACCA 615
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 392 GCGCGCTCTGGCGTGAATGGCCGCTGACATCCGGGTGAAGTCAGCTACAGCC 451
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 616 GTTTACATCTACGGCTTGTGAACTGAAAGATGTATCATGGTAAAGGAATGTACAC 675
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 452 GATACATGCTTACTGGCTGACGGCTGACGGATGTTGCTGAGAACCGGAATGGCGAC 511
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 676 AGATGGACCTGGTACCTACAGAAGATGTCGAACGAAAGGATACHTGGCT 735
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 512 AAGTGGATCTCTCATCCCCACGGCAAGATGGTACTCCGGAGACCTGATGGGCC 571
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 736 GTTTGTACTCTTCTGAA 755
 QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 572 GTTTACCTCTCTCAGTGA 591
 RESULT 13

CO14155 CO14155 CO141255 CO141255 447 bp mRNA linear EST 17-JUN-2004
 Locus EST335926 Aspergillus flavus Normalized cDNA Expression Library
 Definition CO141255 Aspergillus flavus cDNA clone NAFFA37 5' end, mRNA sequence.

ACCESSION CO141255
 VERSION CO141255.1
 KEYWORDS GI:48890246
 SOURCE EST.
 ORGANISM Aspergillus flavus

REFERENCE
 AUTHORS Yu.J., Whitelaw,C.A., Nierman,W.C., Bhatnagar,D. and Cleveland,T.E.
 TITLE Aspergillus flavus expressed sequence tags for identification of

JOURNAL PEMS Microbiol. Lett. (2004) In press
 COMMENT
 Food and Feed Safety Research Unit
 USDA/ARS, Southern Regional Research Center
 1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
 tel: 504 286 4405
 Fax: 504 286 4419
 Email: jiyu@ssrc.ars.usda.gov
 Contract Dr. Yu at USDA/ARS SRRC (jiyu@ssrc.ars.usda.gov) for clone information
 PCR Primers
 FORWARD: M13F
 BACKWARD: M13R
 Seg primer: M13 Forward
 POLA=No.

FEATURES source
 Location/Qualifiers
 /organism="Aspergillus flavus"
 /mol_type="mRNA"
 /strain="NRRL 3357"
 /db_xref="taxon:15059"
 /clone="NFEA37"
 /sex="asexual mycelia"
 /cell_type="mycelia"
 /lab_host="E. coli DH1B T1 resistant cells"
 /clone_libr="Aspergillus flavus Normalized cDNA Expression Library"
 /dev_stages="developmental stages from 18 to 96 hours"
 /notes="vector: pBlueScript (SK+) (stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."

ORIGIN

Query Match 11.9%; Score 97.2; DB 7; Length 447;
 Best Local Similarity 58.7%; Pred. No. 1.4e-16;
 Matches 168; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 464 TGTGTTGATGGTCTATGCTCGGGCCATTGTCACAGATCCTCAAAACAGTGCTCT 523
 Db 162 TTGTCATGATGGTAGCATGTCGGTGCTATCCTCAAGGTGCCAACCCAGGCCTT 221

Qy 524 AGRACATGTCAGGCTGGTGTATCCATTGCTAAGCTTGGCTGATGCTTAACCGGTA 583
 Db 222 ACAGCGCGCAGGGCGCTGTTGTCRACTTGCCGCTCTGGCCATGGCTGGCG 281

Qy 584 AGTACAACATCAGGTTAATCTTAAACCAGGTTACATCTAGGCTCTTGACCGA 643
 Db 282 GRCAGCACATCCGGTCACTCATGCGTACGATGCTACTCCCTGACCGCA 341

Qy 644 ATGTTATCAATGTAACGAAAGATGTTGACAGATGATCTGGTATCCCACCGCA 703
 Db 342 AGATTTGGTAGAGAACCCGGAATGGCGGAGCTGATCTGGCTACCCACCGCA 401

RESULT 14

AU249728 LOCUS AU249728 511 bp mRNA linear EST 22-APR-2004
 DEFINITION AU249728 SL *Lolium multiflorum* cDNA clone SL002A09-5, mRNA
 ACCESSION AU249728
 VERSION AU249728.1 GI:46506997
 KEYWORDS Lolium multiflorum (Italian ryegrass)

ORGANISM *Lolium multiflorum*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Poace; Pooid; *Lolium*.
 REFERENCE 1 (bases 1 to 511)
 AUTHORS Ikeda, S.
 TITLE Unpublished (2004)
 JOURNAL *Lolium multiflorum* EST Project
 COMMENT Contact: Seishi Ikeda
 Japan Grassland Farming Forage Seed Association(JFSA)
 Forage Crop Research Institute(FCRI)
 Higashikada 388-5, Nishinasuno, Tochigi 329-2742, Japan
 Tel: 81-887-37-6755
 Fax: 81-887-37-6757
 Email: sikeda67@jfcass.or.jp
 contact:Tadashi Takamizo (takamizo@affrc.go.jp)
 National Institute of Livestock and Grassland Science, Nishinasuno
 Resistance gene analog location/Qualifiers
 /clone_libr="SL"
 /tissue_type="Powdery mildew infected leaf"

ORIGIN

Query Match 11.4%; Score 93.2; DB 1; Length 511;
 Best Local Similarity 58.5%; Pred. No. 2.1e-15;
 Matches 200; Conservative 0; Mismatches 138; Indels 4; Gaps 2;

Qy 589 AACATCAGGTTAATCTTAAACCGGTTACATCTAGGCTCTTGACCAAGATGGT 648
 Db 122 GGATTCGGTCAATTGCTGGTACATGGCTCACTGGCATTTGACCAAATTAAT 181

Qy 649 A-TCAATGGTACGAGAAATGTCACACAGATGATCTCGTGTATCCACACAAGAT 707
 Db 182 ACTCGAAGAAATCTCTGATTAAGAAGCAATGGATACTCGTATTCGTTACAGGAAAT 241

Qy 708 GTCGAMCAAGGAATACATGGTGTGTTGACTGCTTCGAATCTGCTGTC 767
 Db 242 GGGTAACGAGATGATGGAGCTGGACGAGTACTTGTGCTTCGAA---TGCTCATC 298

Qy 768 ATGACTACTGGCCAGCTACTGGTGTGATGGTGGTTAC 809
 Db 299 ATACATGAGGGCTCATCTAGAGGGATGGGGTACAC 340

RESULT 15

CN811863/c LOCUS CN811863
 DEFINITION Fg09_08p20_A Fg09_MFC_ECOR_Fusarium_Graminearum_simple_substrate
 ACCESSION Gibberella zeae cDNA clone Fg09_08p20, mRNA sequence.
 VERSION CN811863
 KEYWORDS EST.
 SOURCE Gibberella zeae
 ORGANISM Gibberella zeae
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS Watson, R.J., Heyes, R., Couroux, P., De Moors, A., Harris, L.J., Hattori, J., Lacroix, C., Mabotti, M., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D. and Tinker, N.A.

TITLE A cDNA library prepared from *Fusarium graminearum* grown on a simple substrate
JOURNAL Unpublished (2003)
COMMENT

Contact: Watson, Robert J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonj@agr.gc.ca

FEATURES

source

1. .892
Location/Qualifiers
/organism="Gibberella zaeae"
/mol type="mRNA"
/stain="POM 180378"
/db_xref="taxon:5518"
/clone="Fg09_08p20"
/tissue type="mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_id="Fg09_AARC_ECORC_Fusarium_graminearum_simple_substrate"
/notc="Vector: pBluescript II+, Site 1: EcoRI; Site 2:
XbaI; *Fusarium graminearum* grown on a simple substrate--
minimal media supplemented with amino acids."

ORIGIN

Query Match 11.1%; Score 90.8; DB 7; Length 892;
Best Local Similarity 54.5%; Pred. No. 1.2e-14;
Matches 204; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

Qy	437	TCAAGAGGGATCAAGGGTGCCTCTGTGTTGATGGTCTATGTCGTGCCATTG	496
Db	388	TCAATGGAGCCGTCAGGCGCCGTTAGTATGTTGTTATGGAAAGCATGCTCTGGCCATTG	329
Qy	497	TCAACGATCTCTCAAACCAAGTGTCTAACATGTCAGAGCTGGTGTATCCATTG	556
Db	328	TCAATGTCCTCAGGCCAACAGGCCATAAACGGGAAGAACGAGCTGGTGCACCTGG	269
Qy	557	CTTAAAGACTTTGCTTCTGAAATGGCTTAAGTACAATCAGGTTAACTTAAACCCAG	616
Db	268	CAGCTTCTCTTGCACTGGAGTGGGGTCACGGCTGGAAATCGTCAACTGCTCTCTG	209
Qy	617	GTTACATCTACAGCTCTTGAAAGATGTTATCAGGAAAGATGTACACA	676
Db	208	GCTTATATGTTGACTGCTTGACAGAGATCTCGAGAACCTGATTAGAGAA	149
Qy	677	GATGGATCTCTGGTATGCCAACAAAGAATGCCAACAGGAACTTGCTG	736
Db	148	CCTGGACATCCCTCATTCCTTAGGGTGCATGGACTGCCAACGGATTCCTGG	89
Qy	737	TTTGGTACTTCTTCGAAATGCTGCTCTTACACTACTGGTGCAGCTTACTGTTG	796
Db	88	TAACTTCTGCTCATCAGA---TGGCTCATCTATANGACTGGCGAGATTCGAGTTG	32
Qy	797	ATGGTGGTTTACT 810	
Db	31	ATGGAGGATAACT 18	

Search completed: March 2, 2005, 16:54:05
Job time : 3394 secs

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GenCore version 5.1.6

Om nucleic - nucleic search, using SW model

Run on: March 2, 2005, 15:57:37 ; Search time 594 Seconds
(without alignments)

8140.026 Million cell updates/sec

Title: US-10-720-018-1

Perfect score: 816

Sequence: 1 atggatgactacatccaa.....atggtggttcaactcttgg 816

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: d394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0‡

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgmn_6/ptodata/2/pubnra/US07_NEW_PUBCOMB.seq:*

3: /cgmn_6/ptodata/2/pubnra/US07C_PUBCOMB.seq:*

4: /cgmn_6/ptodata/2/pubnra/US06_PUBCOMB.seq:*

5: /cgmn_6/ptodata/2/pubnra/US07_NEW_PUB.seq:*

6: /cgmn_6/ptodata/2/pubnra/US07_PUBCOMB.seq:*

7: /cgmn_6/ptodata/2/pubnra/US08_NEW_PUB.seq:*

8: /cgmn_6/ptodata/2/pubnra/US08_PUBCOMB.seq:*

10: /cgmn_6/ptodata/2/pubnra/US09C_PUBCOMB.seq:*

11: /cgmn_6/ptodata/2/pubnra/US09C_PUBCOMB.seq:*

12: /cgmn_6/ptodata/2/pubnra/US09_NEW_PUB.seq:*

13: /cgmn_6/ptodata/2/pubnra/US10A_PUBCOMB.seq:*

14: /cgmn_6/ptodata/2/pubnra/US10B_PUBCOMB.seq:*

15: /cgmn_6/ptodata/2/pubnra/US10C_PUBCOMB.seq:*

16: /cgmn_6/ptodata/2/pubnra/US10D_PUBCOMB.seq:*

17: /cgmn_6/ptodata/2/pubnra/US10E_PUBCOMB.seq:*

18: /cgmn_6/ptodata/2/pubnra/US10F_PUBCOMB.seq:*

19: /cgmn_6/ptodata/2/pubnra/US10_NEW_PUB.seq:*

20: /cgmn_6/ptodata/2/pubnra/US11_NEW_PUB.seq:*

21: /cgmn_6/ptodata/2/pubnra/US60_PUBCOMB.seq:*

22: /cgmn_6/ptodata/2/pubnra/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGMENTS

RESULT 1

US-10-720-018-1

; Sequence 1, Application US/10720018

; Publication No. US20040132074A1

; GENERAL INFORMATION:

; APPLICANT: Verho, Ritva

; APPLICANT: Richard, Peter

; APPLICANT: Penttila, Marja

; TITLE OF INVENTION: New Enzyme for an in vivo and in vitro utilisation of

; TITLE OF INVENTION: carbohydrates

; FILE REFERENCE: 2330-120

; CURRENT APPLICATION NUMBER: US/10/720,018

; CURRENT FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 816

; TYPE: DNA

; ORGANISM: Ambrosiozyma monospora

US-10-720-018-1

Query Match 100.0%; Score 816; DB 18; Length 816;

Best Local Similarity 100.0%; Pred. No. 2.4e-230;

Matches 816; Conservative 0; Mismatches 0; Index 0; Gaps 0;

Qy 1 ATGACTAATCATTCACATTAGTTAGATCGATGGCCACTAACATGTGCACAGGTGCC 60

Oy 1 ATGACTAATCATTCACATTAGTTAGATCGATGGCCACTAACATGTGCACAGGTGCC 60

6 1 TGGTGTGTTAGCTGAGCTTAATCAAGCTTGTTGCTGCTACGCTTCTGACATGCT 120

7 61 TGGTGTGTTAGCTGAGCTTAATCAAGCTTGTTGCTGCTACGCTTCTGACATGCT 120

8 61 TGGTGTGTTAGCTGAGCTTAATCAAGCTTGTTGCTGCTACGCTTCTGACATGCT 120

9 61 TGGTGTGTTAGCTGAGCTTAATCAAGCTTGTTGCTGCTACGCTTCTGACATGCT 120

10 63 6 8.3 773 17 US-10-369-493-26991 Sequence 26991, A

11 63 6 7.8 774 17 US-10-369-493-25810 Sequence 25810, A

11 60.6 7.4 636 18 US-10-653-047-3866 Sequence 3866, Ap

Sequence 1, Appli

Sequence 3, Appli

Sequence 948, App

Sequence 948, App

Sequence 38959, A

Sequence 38950, A

Sequence 100705, Sequence 339, App

Sequence 1025, Ap

Sequence 1025, Ap

Sequence 26631, A

Sequence 39, Appli

Sequence 53, Appli

Sequence 45, Appli

Sequence 47, Appli

Sequence 51, Appli

Sequence 51, Appli

Sequence 45, Appli

Sequence 47, Appli

Sequence 699, App

Sequence 497, App

Sequence 55, Appli

Sequence 57, Appli

Sequence 113, App

Sequence 119, App

Sequence 43, Appli

Sequence 43, Appli

Sequence 6746, Ap

Sequence 6746, Ap

Sequence 1690, Ap

RESULT 2
 US-10-653-047-41
 ; Sequence 41, Application US/10653047
 ; Publication No. US20040229367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Randy M. Berka
 ; APPLICANT: Michael W. Rey
 ; APPLICANT: Jeffrey R. Shuster
 ; APPLICANT: Sakari Kauppinen
 ; APPLICANT: Ib Groth Clausen
 ; APPLICANT: Peter Bjørke Olsen
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; TIME OF INVENTION: Expression
 ; FILE REFERENCE: 5849_200-US
 ; CURRENT APPLICATION NUMBER: US/10/653, 047
 ; CURRENT FILING DATE: 2003-08-29
 ; PRIOR APPLICATION NUMBER: US/09/533, 559
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/273, 623
 ; PRIORITY FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 7860
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 41
 LENGTH: 3203
 TYPE: DNA

RESULT 3
 US-10-653-047-4932
 ; Sequence 4932, Application US/10653047
 ; Publication No. US20040229367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Randy M. Berka
 ; APPLICANT: Michael W. Rey
 ; APPLICANT: Jeffrey R. Shuster
 ; APPLICANT: Sakari Kauppinen
 ; APPLICANT: Ib Groth Clausen
 ; APPLICANT: Peter Bjørke Olsen
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; TIME OF INVENTION: Expression
 ; FILE REFERENCE: 5849_200-US
 ; CURRENT APPLICATION NUMBER: US/10/653, 047
 ; CURRENT FILING DATE: 2003-08-29
 ; PRIOR APPLICATION NUMBER: US/09/533, 559
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/273, 623
 ; PRIORITY FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 7860
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4312
 LENGTH: 687
 TYPE: DNA

; ORGANISM: *Fusarium venenatum*
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(3203)
 ; OTHER INFORMATION: n = A, T, C or G
 US-10-653-047-41
 Query Match 12.2%; Score 9.4; DB 18; Length 3203;
 Best Local Similarity 52.7%; Pred. No. 4.3e-18;
 Matches 265; Conservative 0; Mismatches 231; Indels 7; Gaps 2;
 ;
 Db 301 TTGCACTGGTTAACACAGCTGTACTGTGAAACTTCCCMGTGAGAGATACCCAGCC 360
 Qy 361 AAGAACCTGAGAAGATGGTGGAGGTACTGTGTTGGCTTGTGATGTTCTCAGCC 360
 Db 361 AAGAACGCTGGAGAGATGGTGGAGGTACTGTGTTGGCTTGTGATGTTCTCAGCC 420
 Qy 421 TTGCTAGGCATGATCAAAGAGCTACAGGGATCTCTGTTGTTGATGTTCT 480
 Db 421 TTGCTAGGCATGATCAAAGAGCTACAGGGATCTCTGTTGTTGATGTTCT 480
 Qy 481 ATGCTCGTGCCATGTCACAGATCTCCAAACCAGCT 540
 Db 481 ATGCTCGTGCCATGTCACAGATCTCCAAACCAGCT 540
 Qy 541 GGTGTTATCCATTGGTAAGACTTGGCTTGATGAACTGACAGTT 600
 Db 541 GGTGTTATCCATTGGTAAGACTTGGCTTGATGAACTGACAGTT 600
 Qy 601 AATCTTAAACCCAGGTACATCTACGGCTTTGACAGGAATGTTATGTCAC 660
 Db 601 AATCTTAAACCCAGGTACATCTACGGCTTTGACAGGAATGTTATGTCAC 660
 Qy 661 GAGAATGTCACACAGTGGAACTCTCGGTCTCCACAAAGAATGTCGAACAAAG 720
 Db 661 GAGAATGTCACACAGTGGAACTCTCGGTCTCCACAAAGAATGTCGAACAAAG 720
 Qy 721 GAAATCATGGCTGCTGATCTCTGGTACATCTCTGGTACATCTACTGGT 780
 Db 721 GAAATCATGGCTGCTGATCTCTGGTACATCTCTGGTACATCTACTGGT 780
 Qy 781 CGCAGCTTACTGGTGTGGTGTACTCTCTGG 816
 Db 781 CGCAGCTTACTGGTGTGGTGTACTCTCTGG 816
 ;

```

; ORGANISM: Aspergillus oryzae
; FEATURE: misc_feature
; LOCATION: (1)..(687)
; OTHER INFORMATION: n = A,T,C or G
; US-10-653-047-4932

Query Match 10.9%; Score 88.6; DB 18; Length 687;
Best Local Similarity 49.8%; Pred. No. 2.8e-15;
Matches 279; Conservative 0; Mismatches 275; Indels 6; Gaps 2;

Qy 196 TCGAAAGAGTCGAANGATGGCTCATGCTGTGATATTGATACCGTT 255
Db 114 TCGAACAAATSCCAACGTCACGCCACTACAGCTGATGTTGCACTCGTC 173
Qy 256 CACAGGGTGTCTCAAGTGTAAAGATTGGTAGTGGCATGCACTGGTAAC 315
Db 174 AACGATGCCCTCCGATATATCTCAGACGGCGAT--CGACAACCTGGCAC 230
Qy 316 ACAGCTGTACTGTGAAACATGCCATGAGATPACCAGCAAGAACCTGAGAAG 375
Db 231 TCGCCGGATTCAGAAACCTGATCCACCTCACGACGGCTGCAAAAG 290
Qy 376 ATGGTGGAGGTTACTGTGGTTCTTGATGTTCTCAACCGTTGCTAGCCATT 435
Db 291 CTTGGGGCGTATGTCGATGAGAACATACTTTCGCAACGGTGTGCAAGC--AC 347
Qy 436 ATCAAAGAGGTACTGTGGTTCTTGATGTTCTCAACCGTTGCTAGCCATT 495
Db 348 CTCATGGAGCCAGGTTCGGCAGCTTGTGATGTTGAGCTGAGATGAGCATT 407
Qy 496 GTCAACGATCTCAAACCAAGTGTCAACATGTCGAAGSGCTGGTATTCATTG 555
Db 408 GACAGCTGCCAGCCAGGCTCTTACAAAGCCGAAGGGCTGTGTGTCACCT 467
Qy 556 GCTAAAGACTTGTGCTTGAAATGGCTAAAGTCAACCTGAGTTATTCTTAACCA 615
Db 468 GCGGGTACTTCGCCGGAGATGGCGGTACGACATGCCGGTGTGCTGAGCCT 527
Qy 616 GGTTACATCTACGGCTTGGCAAGAAGATGTTACATGTAACGAAAGATGTACAC 675
Db 528 CGTACATCTACTGGCTGACCGCAAGATTTGGTAGGAAACCCGGTGTGGGAC 587
Qy 676 AGATGGATCTGTGATCCACAAAGATCTCGACAAAGGATACATGGGTCT 735
Db 588 AAGTGGATCTCGTCATCCCACCGGCAAGATEGGTACTCCGGAGGACTGAGGGTCC 647
Qy 736 GTTTGTACTGTGTTCTGA 755
Db 648 GTTACCTTCTCAGNGA 667

RESULT 4
US-10-369-493-36723
; Sequence 36723, Application US/10369493
; Publication No.: US20030233675A1

GENERAL INFORMATION:
; Sequence 26991, Application US/10369493
; Publication No.: US20030233675A1
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY APPLICATION NUMBER: US 60/360,019
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26991
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Neurospora crassa
; US-10-369-493-26991

Query Match 9.9%; Score 80.6; DB 17; Length 735;
Best Local Similarity 61.8%; Pred. No. 6.7e-13;
Matches 128; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 436 ATCAAAGAGGTACAAAGGTCCTGTTGTTGATGTTGGTCTATGCTGGCATT 495
Db 364 ATCAGTCGCGTGCACACCGCTCATTATCCTTGCTGATGTCGGCACCATC 423
Qy 496 GTCAACGATCTCAAACCAAGTGTGTTACACATGTCACAGCTGCTGGTAAACCATTTG 555
Db 424 GTCAACGATCTCAAACCAAGTGTGTTACACATGTCACAGCTGCTGGTCACTGGCTC 483
Qy 556 GTCAACGATCTGTGCGAGTGGCTGAGTCACAGTGTAAATCTTAACCA 615
Db 484 GCGAACGTCCTGTGCGAGTGGCTGAGTCACATCCGGTAACTGCAATTCCCC 543
Qy 616 GGTTACATCTACGGCTTGGCAAGAAGATCTCGACAAAGGATACATGGGTCT 603
Db 307 GTGCGCACCTGTGCTGCTGCTGCGCTGATGGCGCAGGACATGGTATCAGGGTAAC 366
Db 367 TCGATTGCGTGTGATCATGTGACTGCTG 399

RESULT 5
US-10-369-493-26991
; Sequence 26991, Application US/10369493
; Publication No.: US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY APPLICATION NUMBER: US 60/360,019
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26991
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Neurospora crassa
; US-10-369-493-26991

Query Match 9.9%; Score 80.6; DB 17; Length 735;
Best Local Similarity 61.8%; Pred. No. 6.7e-13;
Matches 128; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 436 ATCAAAGAGGTACAAAGGTCCTGTTGTTGATGTTGGTCTATGCTGGCATT 495
Db 364 ATCAGTCGCGTGCACACCGCTCATTATCCTTGCTGATGTCGGCACCATC 423
Qy 496 GTCAACGATCTCAAACCAAGTGTGTTACACATGTCACAGCTGCTGGTAAACCATTTG 555
Db 424 GTCAACGATCTCAAACCAAGTGTGTTACACATGTCACAGCTGCTGGTCACTGGCTC 483
Qy 556 GTCAACGATCTGTGCGAGTGGCTGAGTCACAGTGTAAATCTTAACCA 615
Db 484 GCGAACGTCCTGTGCGAGTGGCTGAGTCACATCCGGTAACTGCAATTCCCC 543
Qy 616 GGTTACATCTACGGCTTGGCAAGAAGATCTCGACAAAGGATACATGGGTCT 603
Db 307 GTGCGCACCTGTGCTGCTGCTGCGCTGATGGCGCAGGACATGGTATCAGGGTAAC 366
Db 367 TCGATTGCGTGTGATCATGTGACTGCTG 399

```

Db 544 |||||GGTACATGGATACCGCCCTGATAAG 570 ; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; PRIORITY NUMBER: US/09/533, 559
; CURRENT FILING DATE: 2001-08-29
; PRIORITY APPLICATION NUMBER: US/09/734, 237B
; PRIORITY FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4825
; LENGTH: 1146
; ORGANISM: Aspergillus oryzae
; US-10-653-047-4825

Query Match 9.1%; Score 74.6; DB 10; Length 852;
Best Local Similarity 56.0%; Pred. No. 4.3e-11; Matches 209; Conservative 0; Mismatches 149; Indels 15; Gaps 3; Matches 206; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Qy 437 TCAAGAAGGGATCACAGGTGCTTCGTTGTTGATGTTGCTCTATGCTCGGCCATG 496 ; OTHER INFORMATION: Synthetic gene derived from *Candida magnoliae* NADPH-dependent car
; OTHER INFORMATION: bonyl reductase, having numerous codons replaced with others encd
; OTHER INFORMATION: dng the same amino acids to reduce the free energy of folding
; US-09-734-237B-71

Db 485 TCGAAAGGAAGGTAGAAAGGCGCTGGTACATCG 544
Qy 497 TCAACGATCCTCAAACCAAGATGTCACAAAGATGTCACAGCTGGGTAAACATTGG 556
Db 545 TPAACGPACCCAGTTTCAGGCTACCTAACAAAGCTCTAAAGCTGGTGTGACTTCG 604
Qy 557 CTAAAGACTTCGCTTGTAAGCTGGCTAGTACACATCAGTTAATCTTAACCCAG 616
Db 605 CTAATCTCTGCTGTAGAATTCGTCGT--TCGTCGTTAACCTCTTCCTCGG 661
Qy 617 GTTACATCTAGGGCCATTGCAACATGTTATCATGTTAACAGGAGATGTACAAC 676
Db 662 GCTACATCACAC-----ACCGAACATCTTGACTTGTACCGCAGAACATCAGAAC 712
Qy 677 GATGGACTCTCGTATCCACACAAAGATGCCAACAGGATACTTGGTGTG 736
Db 713 ATGGGAGGTCTCTGGTACCGCTGGCGCTGGCAACGCTGACTTGCTGGCTT 772
Qy 737 TTGAGACTCTGCTGAAATGCTGCTCTATACACTACTGGTGCAGCTACTGGTG 796
Db 773 ACCTGTTCTGCTCTGTA--CGCTGTTTACCTACCGCACTGACATCATGTTG 829
Qy 797 ATGGGGTTTACAC 809
Db 830 AGGGGGTACAC 842

RESULT 7
US-10-653-047-4825
; Sequence 71, Application US/10553047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen

RESULT 8
US-10-425-115-172450
; Sequence 177450, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 122450
; LENGTH: 775
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_88858C.1
; US-10-425-115-172450

Query Match ; Score 8.9%; DB 18; length 775;
 Best Local Similarity 56.2%; Pred. No. 1.8e-10;
 Matches 136; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 383 AGTTAACTTGTTGGGTCCTTGTATGTTCAAGCCTTGCTAAGCATGATCAAAG 442
 Db 465 AGTCACGTTGGACAGTGTGGCTTGCTGAAGCGCTGGACTCTGGACAGT 524

Qy 443 AAGGTATGAGGCTGTTCTGTTGATGTTCTATGTTCTGGCCATGTCACG 502
 Db 525 CTCGCTTACGAGGTTCCATGCTCTCCACCTGGCTCATGCTTCCAAATGTCACC 584

Qy 503 ATCTCTAAACCAAGTGTCTCACACAGTGTGGCTTGTTATCCATTGGCTAAGA 562
 Db 585 GTGGCATCCACCGAGTCCTACAGTCAGTGTGGCTCCAGGCTGCSCCTCGTCAAGTGTAAAGC 644

Qy 563 CTGGCTTGATGGCTAGTACACATCGAGTTAACCTTAAACCCAGGTACA 622
 Db 645 AGCTGGCTGTGAGTGGGCCGACAGGTTGAGTCACACGCTCTGCCAGGTAGC 704

Qy 623 TC 624

Db 705 TC 706

RESULT 9
 US-10-369-493-25810 Application US/10369493
 ; Sequence 25810, Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: J8-10(52052).B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIORITY FILING DATE: 2003-02-28
 ; PRIORITY FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; LENGTH: 783
 ; TYPE: DNA
 ; ORGANISM: Schizosaccharomyces pombe
 ; US-10-369-493-25810

Query Match ; Score 8.3%; DB 17; length 783;
 Best Local Similarity 51.2%; Pred. No. 4.8e-09;
 Matches 213; Conservative 0; Mismatches 154; Indels 9; Gaps 2;

Qy 171 CAATACTACTGAGAAGATTGAGGTGAAAGAGTCCAAAGATGGTTCATGGCTG 230
 Db 171 CGAAAGGCTGAAAGAAATGCCAGGCTAATGGCTCAGCTATAGCAAGTG 230

Qy 231 TGATATTCTGATCTGATACCTTCACAGGTTCTGATGTTGCTAAGGATTTGG 290
 Db 231 CGATGTCACATTCCTAAAGGGTAGACATGGCTTGCTGACATTCAAAAGCTTGA 290

Qy 291 TAGTGGCATGACTGGTACACAGCTGTACAGTGTGAAACTTCCATGTGAGA 350
 Db 291 TACTATTGATATGGTGGCCACAAAGGTATTGCACTGGCAGATCGCCATT--GA 347

Qy 351 TTACCCAGGCAAGAACGCTGAGAGATGTGGAGTTACAGCTGTGAACTTCCATGTGAGA 410
 Db 348 CAGACTTACGAGAATTGTGTAATGAAATAAGTCACCTCTCTGTCCTCAAGT 407

Qy 411 TTCTCAAGGCTTGTGCTAAGCCTATGATCAGAGGTTACAGGGTGTCTTGTGTT 470
 Db 408 CGCTCACATGCTGGCCCATCTTCAAAGCAGG-----CCATGGCAGCTGTAGC 461

RESULT 10
 US-10-369-493-26610 Application US/10369493
 ; Sequence 26610, Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052).B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIORITY FILING DATE: 2003-02-28
 ; PRIORITY FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; LENGTH: 774
 ; TYPE: DNA
 ; ORGANISM: Thermotoga maritima
 ; US-10-369-493-26610

Query Match ; Score 7.8%; DB 17; length 774;
 Best Local Similarity 61.4%; Pred. No. 7.3e-08;
 Matches 102; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 472 ATGGTCTATCTGTCGCTATGGCTAACAGTGTCTACAAACATG 531
 Db 436 ATCGCGTCATGTCGCAACATCGTGTACACAAACCTCTAGAAGCAGACGCTAACAGCT 495

Qy 532 TCCAAAGGTGGTTATCCATTGGCTAAGCTTGGCTGTGAATGGCTAAGTACAC 591
 Db 496 TCCAAAGGGTGTGACCATCTCACCGACATCTGCCGCCAGAGGGCCCGTAGGAA 555

Qy 592 ATCAGAGTTAACTTAAACCCAGTTACATCTAGGTCTTGA 637
 Db 556 ATCAGGGTGACAGCAAAAGCCCCGATACATCGAACACCTCTCA 601

RESULT 11
 US-10-653-047-3866 Application US/10653047
 ; Sequence 3866, Publication No. US20040229367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Randy M. Berka
 ; APPLICANT: Michael W. Rey
 ; APPLICANT: Jeffrey R. Shuster
 ; APPLICANT: Sakari Kauppinen
 ; APPLICANT: Ib Groth Clausen
 ; APPLICANT: Peter Bjørke Olsen
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; FILE REFERENCE: 5049.200-US
 ; CURRENT APPLICATION NUMBER: US/10/653,047
 ; CURRENT FILING DATE: 2003-08-29
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIORITY FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 7860
 ; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3866
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; LOCATION: (1)..(636)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-3866

Query Match 7.4%; Score 60.6; DB 18; Length 636;
Best Local Similarity 51.3%; Pred. No. 5e-07;
Matches 194; Conservative 0; Mismatches 175; Indels 9; Gaps 2;
Db 507 TCTTACTCAGTCCTCAAGGTGAAATACTAACATGACAAGTTGGTGAATG 566
Qy 579 GGCTAAGTACACATCAGAGTAATTCCTAACCGAGGTACACTACGGCTTGTAC 638
Db 567 GCCTAAAGACACATGGGTCAATTGCTCGGGAGTCATTAAACCCACTG 626

Query Match 7.4%; Score 60.6; DB 18; Length 636;
Best Local Similarity 51.3%; Pred. No. 5e-07;
Matches 194; Conservative 0; Mismatches 175; Indels 9; Gaps 2;
Db 211 AGCATGGCTTCATATGCTGTGATATTCTGATTAACCGTCACAAAGCTGTGCT 270
Qy 200 AACTCAGTCGCCTATAAACGCTGAGTCGGAAATCAGGAGGATTTGAGGAGGTAAATCCAG 259
Db 271 CAGTGTCTAAGTGTGAGTTGCTGCACTTGACTGGTTAACACAGCTGGTTACTGT 330
Qy 260 CAGATGCTTCAGACTTGCGAGCTGATATTATCGTGTGAC---TCCGGGTCACT 316
Db 331 GAAACTCCATGTGAGGATACCCAGCCAAAGAACGCTGTGAGAGATGGTGGAGGTAC 390
Qy 317 TCCAATATGCCGAGAGACATACACCGAACATGGCGACATCATGGGCAAT 376
Db 391 TCTTGTGGTTCTTGTGTGTTGATGCTGCTCAAGCCTTGTCTAGCATTGATCAAGAGGTATC 450
Qy 377 CTAGATGGCGCAATTATAGCGGGCACGGCTTCTGGGATCTCAAGAACAGG---- 432
Db 451 AAGGTGCTCTCTGTTGTTGATGCTGCTGCTGCAATTGCAAGAGGTCTCAA 510
Qy 433 --ACATGGAAATGTAATCCTACAGCCTGTCAGTCACATGGGAATGTGCCCAG 490
Db 511 AACCAAGTGTCTACAAAGATGTCAGCTCAAGCTGGTGTATCCATTGGCTAACACTTGCT 570
Qy 491 AAGCAAGCTGCTACAAAGCTGGCTGCTGCAATGGCAAATGTCTGTCT 550
Db 571 TGTAATGGCTAAAGCTGGGTCTGCAAATGGCAAATGTCTGTCT 588
Qy 551 GTGGAATGGTGTGANTC 568

Db 807 T 807

RESULT 12
US-10-314-394-1

; Sequence 1, Application US/10314394
; Publication No. US20030143700A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroaki
; APPLICANT: Ueda, Momoko
; APPLICANT: Pan, Ritsuzui
; APPLICANT: Hamatani, Takeshi
; TITLE OF INVENTION: METHODS FOR PRODUCING OPTICALLY ACTIVE ALCOHOLS
; FILE REFERENCE: SHZ-006
; CURRENT APPLICATION NUMBER: US/10/314, 394
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/385, 434
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: JP 2002-152955
; PRIOR FILING DATE: 2002-05-27
; PRIOR APPLICATION NUMBER: JP 2001-375041
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SSO ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Hyoscyamus niger
US-10-314-394-3

Query Match 6.9%; Score 56.4; DB 15; Length 825;
Best Local Similarity 52.4%; Pred. No. 1e-05;
Matches 151; Conservative 0; Mismatches 131; Indels 6; Gaps 1;
Db 532 TCCAAGCTGCTGTTATCCATTGGCTAACACTTGCTGTGATGGCTAATGAC 591
Qy 523 TCCAAAGCTGCTAACATATCAAAACGAGACTGCTGGCATGTGGCAGAAC 582
Db 592 ATCAGAGTTATTCTTAACCCAGGTACATCAGCTGCTTGACGAGAAGTTAC 651
Qy 583 ATTGGGTCAATTCTGCTCAGGTCATTAAACCCACACTATGAACTGCAATT 642
Db 652 -----ATGCTAACGAGATGTGACACAGATGATGCTCTGGTATCCCACAAAGA 705
Qy 643 AAGAAATTCATCAAAAGAGAATGACAAATTATGCTAACACTCCATGGC 702
Db 706 ATGTCGCAACCAAAAGATACTATGGTGTGTTGACTTGCTTCTGATCTGCT 765
Qy 703 CGGGCTGAGAACCCATGAGGTGCTGCACTAAATGCCCTCTGCTCCCTGCTGCT 762
Db

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Query Match 7.3%; Score 59.8; DB 15; Length 822;
Best Local Similarity 52.5%; Pred. No. 1e-06;
Matches 158; Conservative 0; Mismatches 137; Indels 6; Gaps 1;

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; ; PRIOR APPLICATION NUMBER: US 60/264, 647
; ; PRIORITY FILING DATE: 2001-01-16
; ; PRIORITY APPLICATION NUMBER: US 60/300, 111
; ; PRIORITY FILING DATE: 2001-06-22
; ; NUMBER OF SEQ ID NOS: 5379
; ; SEQ ID NO: 948
; ; LENGTH: 789
; ; TYPE: DNA
; ; ORGANISM: Arabidopsis thaliana
; ; US-09-938-842A-948
; ; Sequence 948, Application US/09938842A
; ; Publication No. US20040009476A9
; ; GENERAL INFORMATION:
; ; APPLICANT: Harper, Jeff
; ; APPLICANT: Kreps, Joel
; ; APPLICANT: Wang, Xun
; ; APPLICANT: Zhu, Tong
; ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; ; TITLE OF INVENTION: SAME, AND METHODS OF USE
; ; FILE REFERENCE: SCIP1100-3
; ; CURRENT APPLICATION NUMBER: US/09/938, 842A
; ; CURRENT FILING DATE: 2001-08-24
; ; PRIOR APPLICATION NUMBER: US 60/227, 866
; ; PRIOR FILING DATE: 2000-08-24
; ; PRIOR APPLICATION NUMBER: US 60/264, 647
; ; PRIOR FILING DATE: 2001-01-16
; ; PRIOR APPLICATION NUMBER: US 60/300, 111
; ; PRIOR FILING DATE: 2001-06-22
; ; NUMBER OF SEQ ID NOS: 5379
; ; SEQ ID NO: 948
; ; LENGTH: 789
; ; TYPE: DNA
; ; ORGANISM: Arabidopsis thaliana
; ; US-09-938-842A-948

Query Match 6.9%; Score 56.2; DB 11; Length 789;
Best Local Similarity 55.2%; Pred. No. 1.1e-05;
Matches 153; Conservative 0; Mismatches 118; Indels 6; Gaps 2;
Query 533 CCAGGGCTGGTTATCCATTGCTTAAGACTTGTGCTTGATGGCTTAAGTACACA 592
Db 485 CAAAGGAGCTTGATCAGCTAACATGGCTAAATTGGCATGTCATGAAAGGGCA 544
Query 593 TCGAGTTAACTCTTAACCCAGGTTACATCTACGGGCTTGTGACCAAGATGTTCA 652
Db 545 TAGAGGCCAACCTGGTGCCTTAATGTCATGAACTCTCTGTCATCTATCTTG 604
Query 653 ATGGTACAGGAAATTCACACAGATGGATCTCTGTATCCACACAAAGATGCC 712
Db 605 AGG---ACGTCAATTGAGGGCTTGTGAGTAGCTCCACTCTGTCGTGAG 661
Query 713 AACCAAGGAATACATGGTGTGTTGTACTGTCTCTGAATCTGCTGCTCATACA 772
Db 662 ACCAAATGAG---TGGCATACTGGCTCTGTGTGACCTACCGACCTCTATA 718
Query 773 CTACTGGCAGCTCTGGTGTGGTTAC 809
Db 719 TTACTGGCAGACTATTGTGTGAGGCTCTCAC 755

Search completed: March 2, 2005, 18:17:37
Job time : 597 secs

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RESULT 15
US-09-938-842A-948
; Sequence 948, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCIP1100-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2005, 11:05:37 ; Search time 185 Seconds

(without alignments) 7217.307 Million Cell updates/sec

Title: US-10-720-018-1

Perfect score: 816

Sequence: 1 atggatgactacatccaac.....atgggtgttcacttcttg 816

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cggn_6/ptodata/1/ina/5A_COMB.seq: *

2: /cggn_6/ptodata/1/ina/5B_COMB.seq: *

3: /cggn_6/ptodata/1/ina/6A_COMB.seq: *

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5: /cggn_6/ptodata/1/ina/PCTUS_COMB.seq: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	230.2	29.2	696 2	US-08-336-198C-6
2	238.2	29.2	696 4	US-08-180-555-5
3	218.6	26.8	846 4	US-09-243-7960-29
4	86.6	10.6	927 4	US-09-243-7960-2490
5	74.6	9.1	4 4	US-09-734-327B-71
6	61.8	7.6	873 4	US-09-248-7960-2654
7	55.1	6.7	336 4	US-09-248-7960-2488
8	53	6.5	372 4	US-09-248-7960-5987
9	53	6.5	774 3	US-09-130-001C-725
10	51.8	6.3	825 4	US-09-243-796A-2730
11	51.2	6.3	3 3	US-09-367-012-2
12	51.2	6.3	852 3	US-09-777-157B-2
13	51.2	6.3	852 4	US-09-734-237B-69
14	51.2	6.3	951 4	US-09-489-039A-5819
15	51.2	6.3	1303 3	US-09-367-012-B
16	51.2	6.3	1303 3	US-09-777-157A-B
17	50.4	6.2	441529 3	US-09-03-840B-1
18	49.8	6.1	873 4	US-09-248-796A-2489
19	48.2	5.9	3993 4	US-09-710-279-3985
20	47.4	5.8	440765 3	US-09-03-840B-2
21	47	5.8	732 3	US-09-130-01C-1675
22	45.2	5.5	2774 3	US-09-363-189B-5
23	44.4	5.4	1248 4	US-10-024-816-7
24	43	5.3	879 3	US-09-468-738A-1
25	43	5.3	879 3	US-09-940-019-1
26	43	5.3	4 4	US-09-940-037-1
27	43	5.3	891 3	US-09-468-738A-22

ALIGNMENTS

RESULT 1	US-08-336-198C-6
; Sequence 6, Application US/08336198C	; Patent No. 5866382
; GENERAL INFORMATION:	
; APPLICANT: Haliborn, Johan	
; APPLICANT: Parttila, Merja	
; APPLICANT: Ojamo, Heikki	
; APPLICANT: Kernan, Sirkka	
; APPLICANT: Hahn-Hagerdal, Barbel	
; APPLICANT: Walfridsson, Mats	
; APPLICANT: Airksinen, Ulla	
; TITLE OF INVENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS	
; NUMBER OF SEQUENCES: 9	
; CORRESPONDENCE ADDRESS:	
; ADDRESSEE: Birch, Stewart, Kolasch & Birch	
; STREET: 301 N. Washington St.	
; CITY: Falls Church	
; STATE: Virginia	
; COUNTRY: USA	
; ZIP: 22046-3487	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Floppy disk	
; COMPUTER: IBM PC compatible-MS-DOS	
; OPERATING SYSTEM: PC-DOS/MS-DOS	
; SOFTWARE: Patentin Release #1.0, Version #1.25	
; CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/08/336,198C	
; FILING DATE: 03-NOV-1994	
; CLASSIFICATION: 435	
; ATTORNEY/AGENT INFORMATION:	
; NAME: Murphy Jr., Gerald M.	
; REGISTRATION NUMBER: 28,977	
; TELECOMMUNICATION INFORMATION:	
; TELEPHONE: 703-205-8000	
; TELEFAX: 703-205-8050	
; TELEX: 248345	
; INFORMATION FOR SEQ ID NO: 6:	
; SEQUENCE CHARACTERISTICS:	
; LENGTH: 696 base pairs	
; TYPE: nucleic acid	
; STRANDEDNESS: double	
; TOPOLOGY: linear	
; MOLECULE TYPE: cDNA	
; HYPOTHETICAL: NO	
; ORIGINAL SOURCE:	
; ORGANISM: Pichia stipitis	
; STRAIN: CBS-6054	
; FEATURE:	
; NAME/KEY: CDS	

LOCATION: 1 .. 693
 OTHER INFORMATION: /standard_name= "xylitol"
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PI 901771
 FILING DATE: 06-APR-1990
 US-08-336-198C-6

Query Match 29.2%; Score 238.2; DB 2; Length 696;
 Best Local Similarity 64.4%; Pred. No. 9.4e-65; Mismatches 203; Indels 3; Gaps 1;
 Matches 373; Conservative 0; Mismatches 203; Indels 3; Gaps 1;

QY 227 CCTGTGATATTCTGATCTGATACCCCTCACAGGGTTCTCAAGTCCTAAGTCCTAAGGATT 286
 Db 107 CCTGCAACATCGGGATGCTGAGGCTACTTCAGCTCATCACGACACC 166
 QY 287 TTGTAAGTGCATGCACTTGTTAACACAGCTGGTTAAGTGTAAACACTCCAGTG 346
 Db 167 AGGGCAAGATCGCTGACTTGTTAACACGGCTGAACTCCAGTG 226
 QY 347 AAGATTACCCAGCCAAGAACGCTGAGAGATGCTGAAGGTAACTTGTTGCTCTTGT 406
 Db 227 AACGTAACCGGCTACTAACGCTGAAACCATCATGAAGGTTGGCTCATCT 286
 QY 407 ATGTTCTCAAGGCTTGCTAACGGCTGAAAGGATCAAGGCTGAACTCCAGTG 226
 Db 287 ACATTCGCACTGTCGCTAGCATGAGGATCCAGAAGCTACATGAAAGGTTGGCTCATCT 343
 QY 467 TTGTAAGTGGCTATGCTGGCCATTGICAACGATCTCAACCAAGTGCTACA 526
 Db 344 TCTGTGATGGCTCAATGTCATGTCATGAACTACGACCCACACGCCAAGTGTACA 403
 QY 527 ACTGTCGAAAGGTGGTTATTCATTTGGCTAACACTTGTGAAATGGCTTAAGT 586
 Db 404 ACATGTCGAAAGCTGGAGTCACTTGTCAGATGTTGCTGCGATGGCCAGT 463
 QY 587 ACACATCAGAGTTAATCTTAAACCCAGGTTACATCTAGCTGTTGGCTAAGAT 646
 Db 464 ACACATCAGAGTCACACCTTATCACCAGCTATTCATCTCCCTAAACGAAACG 523
 QY 647 TTATCATGGTAAAGAAATGTCACACAGGATCTCTGGTATCCACACAAAGAA 706
 Db 524 TGATTCCTGGCCACAGAGTGAAGGAGCTGGGATCCAGATCCCAATGAGAA 583
 QY 707 TGTCCGAAACCAAGGAAATACATGGTGTGTTGACTCTGCTGAATCTGCTT 766
 Db 584 TGGCGAACCCAGGATTCGGGGTCATCTTAAACTTSGCAAGGAGCTGCTT 643
 QY 767 CTACACATGCTGGCCAGCTTACTGGTGTGGT 805
 Db 644 CCTACACTACGGGCCACATTTGGTGGAGGAGAT 682

RESULT 2
 US-09-184-965-6
 Sequence 6 Application US/09184965
 Patent No. 658294
 GENERAL INFORMATION:
 APPLICANT: Hallborn, Johan
 APPLICANT: Penttila, Merja
 APPLICANT: Ojamo, Heikki
 APPLICANT: Kervanen, Sirkka
 APPLICANT: Hahn-Hagerdal, Barbel
 APPLICANT: Waldridsson, Mats
 APPLICANT: Airaksinen, Ulla
 TITLE OF INVENTION: Xylose Utilization by Recombinant Yeasts
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Birch, Stewart, Kolasch & Birch
 STREET: 301 N. Washington St.
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA

ZIP: 22046-3487
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/184,965
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA: US/08/336,198
 APPLICATION NUMBER: US/08/336,198
 FILING DATE: 03-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8050
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 696 base pairs
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE: *Pichia stipitis*
 ORGANISM: *Pichia stipitis*
 STRAIN: CBS-6054
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..693
 OTHER INFORMATION: /standard_name= "xylitol"
 OTHER INFORMATION: dehydrogenase
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PI 901771
 FILING DATE: 06-APR-1990
 US-09-184-965-6

Query Match 29.2%; Score 238.2; DB 4; Length 696;
 Best Local Similarity 64.4%; Pred. No. 9.4e-65; Mismatches 203; Indels 3; Gaps 1;
 Matches 373; Conservative 0; Mismatches 203; Indels 3; Gaps 1;

QY 227 CCTGTGATATTCTGATCTGATACCCCTCACAGGGTTCTCAAGTCCTAAGTCCTAAGGATT 286
 Db 107 CCTGCAACATCGGGATGCTGAGGCTACTTCAGCTCCATCACGACACC 166
 QY 287 TTGTAAGTGGCTATGCTGGCCATTGICAACGATCTCAACCAAGTGCTACA 526
 Db 167 AGGGCAAGATCGCTGACTTGTTAACACGGCTGAACTCCAGTG 226
 QY 347 AACGTAACCCAGGCTGGAGTCACTTGTCAGATGTTGCTGAAACTCCAGTG 586
 Db 227 AACGTAACCCAGGCTGGAGTCACTTGTCAGATGTTGCTGAAACTCCAGTG 286
 QY 407 ATGTTCTCAAGGCTTGCTAACGGCTGATCTGAAAGGATTCAGGGCTCTGCTG 466
 Db 344 TCTGTGATGGCTCAATGTCGACATGTCAGCTGAAACCCACACGATCT 403
 QY 527 ACATGTCAGGCTGGTAACTTGCTGAAACTTGCTGAAAGGCTGAGT 586
 Db 404 ACATGTCAGGCTGGTAACTTGCTGAAACTTGCTGAGT 463
 QY 587 AACACATCAGAGTTAATCTTAAACCAAGGTTACATCTAGGGCTCTGACCAAGATG 646
 Db 464 AACACATCAGAGTCACACCTTATCACCAGCTATTTGACTCTTAAACGAAACG 523

RESULT 3
US-09-248-796A-29
; Sequence 29, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 10196-132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY FILING DATE: 1998-02-13
; PRIORITY APPLICATION NUMBER: US 60/074, 725
; PRIORITY FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 29
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-29

Query Match 26.8%; Score 218.6; DB 4; Length 846; Best Local Similarity 62.0%; Pred. No. 1.6e-58; Matches 385; Conservative 0; Mismatches 224; Indels 12; Gaps 2;

Qy 14 TTCAACTTGTAGTCATGGGCACTAACATTGTCACAGTGCTGTGGTTAG 73
Db 218 TCCAACTTCAASGGTTGTTGGATGAAACCTGTTATTAACCGTGGCTCTGGTTGG 277
Qy 74 CTGAAGCTTTAATCAACGGTTGTTGGATGAAACCTGTTATTAACCGTGGCTCTGGTTGG 277
Db 278 CTGCCGTTGATCAGAGCTTATTAGCCAAAGGTGGCATGTTGATTAGCTGATGA 337
Qy 134 ACCAAGAAAGACTGCGCCAAACAACCGAAATACCAAAAGCTGACTGAGATGA 193
Db 338 ACTTGGAAAGAACACAACAAAGCTGAGACTCTTACATGGGCAAAGCAATGA 397
Qy 194 AGTGAAGAAGTTCGA-----AGATGGGTATAGCTGTGATATTCTGAT 244
Db 398 AAGGATAATACGATCACCAATCGTAGGTTGCTGATGTTGCGATGAAATGGCGAT 457
Qy 245 CTGATACCGTTCACAAAGGTGCTGAGATGCTTAAAGGATTGTTGAGTGCCTG 304
Db 458 CTGAGCTGTCGACTTGACATTCAGCCATCACAGCACACCGCAAAATCTCAAGT 517
Qy 305 ACTGTTGTTAACACAGCTGTTACTGTGAAACCTCCATGTAAGATAACCGCAAGA 364
Db 518 TCTGGTCAACACTGGCGTGTACGTGAAACTTCCCAGCTGAGAATGCCAGA 577
Qy 365 ACCTGAGAGATGGTAGGTTACTGTGTTGCTTGTGTTCTCAAGCTTGTG 424
Db 578 AGCTGTGAAACCTTATGAACTTACCGTGGCTGG 637
Qy 425 CTAGGCGATTGTCAGAGGTATCGGGTCTCTGTTGATGGTTCTAGT 484
Db 638 CTGAGCATTAACTCCAAA---CAACATGACCGATGATCATTGATCGGGTCAATGT 694
Qy 485 CTGGTGCATTCITCAAGATCTTCAAAACCAAGTGTCTACACAGTCAGCTGGT 544

RESULT 4
US-09-248-796A-2490
; Sequence 2490, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 10196-132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY FILING DATE: 1998-02-13
; PRIORITY APPLICATION NUMBER: US 60/074, 725
; PRIORITY FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 2490
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-2490

Query Match 10.6%; Score 86.6; DB 4; Length 927; Best Local Similarity 52.0%; Pred. No. 8.1e-17; Matches 328; Conservative 0; Mismatches 279; Indels 24; Gaps 5;

Qy 182 CTGAAAGATTGAGTGGAAAGAGTTCAGAAGATGGGTTCATATSCCTGTGATATTCTG 241
Db 308 CTGAAATTAAACAAAGCTTATGGGGTTAAATCCAACATACAAATGTATGTTACTG 367
Qy 242 ATTCTGATACCTTCACAGGTTGTTCTCAAGTGTGTTAAGGATTTGGTAGTGGCCT 301
Db 368 ATTTCAGATGTTGAAAGAAGTGTGAAACAAATGACTGGATTGGTACATTGATA 427
Qy 302 TGACTTGTGTTACACAGCTGTTACTG---TGAAGACTCCATGTGAAAGTATCCAG 358
Db 428 TCTTGTGCGGATGTGGTGTGCTGGACGGAAGGCCGAATGGATGTCAGGG 487
Qy 359 CCAGAAAGCTTACAGATGGTAACTTGTGGGTTCTCTGTATGTTCTCAAG 418
Db 488 TGCACATGGACAAAGTGTGTTGTTGTTGTTGTTGTTGCTGCTATG 547
Qy 419 CCTTGTGTTACGGATTCATCAAGAGTCAAGGGTCTCTGTTGTTGTTGTTGTTG 478
Db 548 TTTTGTGTCACATTTCAGAAAAGGTA-----AAGGGTCATTCATTTCAGCCA 601
Qy 479 CTAGTGTGGTCACTGTCACAGTCCTCAACACCGATGTTGCAACAGTGTCCAGG 538
Db 602 GTATGCGCTTCATGTTATGTCACATTCAAGACGCTTCAACGCTGPAAG 661
Qy 539 CTGGTGTATCCATTGCTAACGTTGCTTGTGTTGATGGGCTAAAGTACACATCGAG 598
Db 662 CTGGGTCAACGTTGTCACATCATGTTGAGTGTGATGGCCACCTTGT----AGAG 718
Qy 599 TTAATCTTAAACCAAGGTACATTCACGTCGTTGTTGACGAGAATGTTATCAATGTA 658
Db 719 TCAATTGTTCTCCGGTTACATCCTACATCTAGTGAATTTGCTG----- 769
Qy 659 AGGAGATGTCACAGATGATCTCTGTTGACGAGAATGTCGGAACCAA 718
Db 770 ATCCGGATGTCACAGATGTCACACCTGGTCAACACTTGTGAGAAGGCCAACCAA 829

Qy 719 AGGAATACATGGCGTTTGACTGCTTCGAATCGCTGTCAACACTG 778
 Qy |||||
 Db 830 GAGAGCTGTTGCTGCTACTGTTTGGCTCCGA--TGCTCATCTTACACTG 886
 Qy 779 GTGCCAGCTTCTGGTGTGATGGTGTTCAC 809
 Db 887 |||||GATCTCTGTTGATGGTGTAC 917

RESULT 5
 US-00-734-237B-71
 ; Sequence 71, Application US/09734237B
 ; GENERAL INFORMATION:
 ; APPLICANT: Rozzell, J. David
 ; APPLICANT: Bui, Peter
 ; APPLICANT: Hua, Ling
 ; TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
 ; FILE REFERENCE: B583:0608
 ; CURRENT APPLICATION NUMBER: US/09/734, 237B
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 09/494, 921
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 71
 ; LENGTH: 852
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic gene derived from *Candida magnoliae* NADPH-dependent carboxyl reductase, having numerous codons replaced with others encoding
 ; OTHER INFORMATION: dng the same amino acids to reduce the free energy of folding
 ; OTHER INFORMATION: us-09-734-237B-71

Query Match 9.1%; Score 74.6; DB 4; Length 852;
 Best Local Similarity 56.0%; Pred. No. 4.7e-13;
 Matches 209; Conservative 0; Mismatches 149; Indels 15; Gaps 3;

Qy 437 TCAAGGAGGATCAAGGTCCTCTGTTGTTGATGTTCTAAGTCTGGCCATG 496
 Db 485 TTGAAAGGAGGTAAGAACACCGCTCTGGTTACCGCTCTATGCTCAGATC 544
 Qy 497 TCAACGATCTCAAACCAAGTGTCTCACACATGTCACAGCTGAGTTACCATGG 556
 Db 545 TTAACGTTACCGCTACTACATCACAAAGCTGCTAAAGCTGGTTGCTACTTCG 604
 Qy 557 CTAGACTTGCTGTGAACTGGCTAAGTACACTCGAGTTAATCTTAACCCAG 616
 Db 605 CTAATCTCTGCTGAGAATTGCTCGT--TCCCTGTTAACTCTGTTCCCG 661
 Qy 617 GTTACATCTACAGTCCCTGACCAAGAAGTGTATCATGGTACAGAGAATGTACAA 676
 Db 662 GCTACATCACAC-----ACCGAACTCTGACTTGACCCGAGAACATCAGACA 712
 Qy 677 GATGGAACTCTGTTCTGAACTGCTGCTTATACACTGGTGCAGCTTACTGGTG 736
 Db 713 ATGGGTTGCTCTGGTACCGTGGCGGGCTGGGGCAACTCTGACTGGTGGGTT 772

Query Match 7.6%; Score 61.8; DB 4; Length 873;
 Best Local Similarity 51.3%; Pred. No. 5.3e-09;
 Matches 256; Conservative 0; Mismatches 222; Indels 21; Gaps 4;

Qy 307 TGGTTAACACAGCTGTTACTGTGAAACCTCCATGTCAGAGATACCAGCCAGAAC 366
 Db 364 TTGTCATATGCAAGAACTAAAGATCCATGCTCAGATTTCCACAACTAAG 423
 Qy 367 GCTGAGAGATGGAGGTACTGTGGTCTTGTGATGTTCTGAGCTTCAGCCCTGCT 426
 Db 424 TTGATGACGCGTATAAGTTGATGTTAATTCCGGTAAGTGTACTAAAGCTATTGGT 483
 Qy 427 AAGCCATGTATCAAGAAGGTTACATCAGGGCTCTGTTGTTGATTGTTTACCGCTTATAC 486
 Db 484 AGGAATATGCTGAAACAAATTACCAAGGGTAGATTGTTTACCGCTTATAC 542
 Qy 487 GGTGCCTATGTCAGATCCCTAACACCAAGTGTGTTACACAGTCACAGCTCAGGCTGTT 546
 Db 543 -ATTCGAGGGAGTGTGTCAGCCCC-----CTATCCATCAGTAAAGGTCCTTA 594
 Qy 547 ATCCATTGGCTAAGACTTGGCTGATGGCTAATCACACATCAGAGTATTCT 606
 Db 595 AAACATTCACAAAGAAGTATCTATGATGTCATCAAGGGTATCAGGTCAATCA 654
 Qy 607 TTAACCCAGGTTACATCTAGGTCTTACCHAGAATGTTATGATGTAACAGAA 666
 Db 655 ATTGCACTGATAATCAAACCAATTGCGACAGCAGCTGAGAAGAACAGAAA 714
 Qy 667 TTGTCACACAGATGGTCTTGTGTTCCACAAAGAAGTGTGTCGAGAACAAAGAAC 726
 Db 715 ATGGTGTAT-----TGAGAATCCCTAGTAAAGAAGTGGGTAACCGAGACCTT 765
 Qy 727 ATGGCTGCTGTTGACTGCTCTGTAATCTGCTGCTTCATACACTTGCGGCCAG 786
 Db 766 ATGGGCAATGTCTTACATCTGA--TGATCGAAATATGTTACTGGTGACACA 822
 Qy 787 TTACTGGTGAATGGGGTT 805
 Db 823 TTATTTGATGGGGTT 841

RESULT 7
 US-00-248-796A-2488
 ; Sequence 2488, Application US/09248796A
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248, 796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074, 725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096, 409
 ; PRIOR FILING DATE: 1998-08-13

RESULT 6
 US-00-248-796A-2654
 ; Sequence 2654, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 2488
; LENGTH: 336
; TYPE: DNA
; ORGANISM: *Candida albicans*
; US-09-248-796A-2488

Query Match 6.7%; Score 55; DB 4; length 336;
Best Local Similarity 52.9%; Pred. No. 4.3e-07; Mismatches 140; Indels 12; Gaps 2;
Matches 171; Conservative 0; MisMatches 140; Indels 12; Gaps 2;

Qy 491 CCATGGTCAACGATCTCAAACCGACTGCTCACACATGCCAACGGCTGGTGTATCC 550
Db 20 CCCGGGTGATACTCCCTAACTACAGCTGCTCACACATGCCAACGGCTGGTGTATCC 79
Qy 551 ATTCGCTAAGACTTGTGGCTGTGAATGGCTAACTACAACATCGAGTTAATTCTAA 610
Db 80 ATTGAGCCTAAATCATGAGCTGGATGGCTAGTTGGCTAGTTGAGTAATTCAATT 139
Qy 611 ACCGGGTACATCACGSPCTTGACCAAGAAGTTATCAAGTGTAAAGGATGTT 670
Db 140 CTCCGGGTATATA-----TTGACTGATATTGTGATTCTGTATCCAGAATGA 190
Qy 671 ACAACAGATGGATCTGGTATCCACACAAAGAATGTCGACGCAAGGATCATG 730
Db 191 AAAAGAAATGTCGCAATGACACTTGGAAAGGATACACAGAAATTAGTGG 250
Qy 731 GTGCTGTTGTACTGTGTTCTGTGATCTCTGTCTCATCACTACTGGGCCACCTAC 790
Db 251 GGCGTATTTACTGGCTC--AAATGCTACATRACTGGTCAATTATGG 307
Qy 791 TGTGTGATGGTGTCACTCT 813
Db 308 CTGTTGATGGGGTATACATGT 330

RESULT 8
US-09-48-796A-6987/C
Sequence 6987, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.12
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY NUMBER: US 60/074, 725
; PRIORITY FILING DATE: 1998-03-13
; PRIORITY NUMBER: US 60/096, 409
; PRIORITY FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 6987
; LENGTH: 372
; TYPE: DNA
; ORGANISM: *Candida albicans*
; US-09-248-796A-6987

Query Match 6.5%; Score 53; DB 3; Length 774;
Best Local Similarity 47.8%; Pred. No. 3e-06; Mismatches 235; Indels 9; Gaps 2;
Matches 223; Conservative 0; MisMatches 235; Indels 9; Gaps 2;

Qy 200 AGAAAGTTCACAGATGGTCATATGCCCTGTGATATTCTGTATCCGGTCACA 259
Db 182 ATACGGTGTAAACACATCATTAATAGATTAACCTCATCTAGATGAGTAATC 241
Qy 260 AGGTGTGTCGAAGTGTAGATTGTAGTTGCTGTCATGCTGCACTGGTAAACAG 319
Db 242 AAATTGGTGTATGAGTAATGGAAATATGGAAAATAGATTAACCTCATCTAGATGAGTAATC 298
Qy 320 CGGGTACTGGAAACCTCCATGAGTTACCGCCAGAACGGCTGAGAGTGG 379
Db 299 CTAGTATCTCAATCAGATGATACTGAAATTGTTGAGGATGTTAAAGAAA 358
Qy 380 TGAAGGTAACTGTGTTGGTCTTGTATGTTGCTGTCATGCTGTCATGTTGCA 439
Db 359 TCAATTAACTTAAATGGAGGATCTGAGCTGAGGCAACACTAGGAGCTGAGTGG 418
Qy 440 AGAAAGGTATCAAGGGCTCTGTGTTGTTGAGGTCTGTCATGCTGTCATGTC 499
Db 419 AGAAGGCA-----GTGGTGTGATGATTAATGTCCTCTCGTATPAGGATGATGCTA 472
Qy 500 AGGATCTCAAACACCAGTTCTACACATGTCGACAGCTGGTATCCATTGGCTA 559
Db 473 ATAAACCGCAAGACCAAGAGCTCTTATGAGCTAAAGCGGTGAGCTGACTA 532
Qy 560 AGACTTGGCTGTGATGCTCTAACATCACATGAGTTAATTCTTAACCCAGTT 619
Db 533 AAGCTTAGCTAGAGATGGCTGATGATGGAAATTAGTGAATGCATTCGCCCTGGTT 592
Qy 620 ACATCTACGGCTTGCACCAAGATCTTACATGTAAGGAGA 665
Db 593 ACATGAGAACATCGAACGAAACGAAAGATACTAAATGTAATGAA 639

RESULT 10
US-09-248-796A-2730
; Sequence 2730, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13 ; TITLE OF INVENTION: No. 6218561 carbonyl reductase, gene coding same, and method
; PRIORITY APPLICATION NUMBER: US 60/096,409 ; TITLE OF INVENTION: For using such reductase and gene
; NUMBER OF SEQ ID NOS: 28208 ; FILE REFERENCE: S72050PCUS
; SEQ ID NO 2730 ; CURRENT APPLICATION NUMBER: US/09/367,012
; LENGTH: 825 ; CURRENT FILING DATE: 1999-11-24
; ORGANISM: Candida albicans ; EARLIER FILING DATE: 1997-09-01
; US-09-248-796A-2730 ; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.1 ; SEQ ID NO 2
; LENGTH: 852 ;
; TYPE: DNA ;
; ORGANISM: Candida magnoliae ;
; US-09-367-012-2
; TYPE: DNA ;
; ORGANISM: Candida magnoliae ;
; US-09-777-157A-2
; Sequence 2, Application US/09777157A
; Patent No. 6448052
; GENERAL INFORMATION:
; APPLICANT: Yashohara, Yoshihiko
; APPLICANT: Kizaki, No. 6448052iyuki
; APPLICANT: Hasegawa, Junzo
; APPLICANT: Wada, Masaru
; APPLICANT: Shimizu, Sakayu
; APPLICANT: Katoka, Michiniko
; APPLICANT: Yamamoto, Kazuhiko
; APPLICANT: Kawabata, Hiroshi
; APPLICANT: Kita, Keiko
; TITLE OF INVENTION: Carbonyl Reductase Enzyme and Methods for its Use
; FILE REFERENCE: 06833.010
; CURRENT APPLICATION NUMBER: US/09/777,157A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/367,012
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Candida magnoliae
; US-09-777-157A-2
; Query Match, Score 51.2; DB 3; Length 852;
; Best Local Similarity 58.6%; Pred. No. 1.2e-05; Gaps 0;
; Matches 89; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
; QY 437 TCAAGAGGTATCAGGGCTTCCTGTTGATGGTCTATGCTGGCATTC 496
; Db 485 TCGAGAGGGCAGAGGGCCCTTGTCACGCCCTCAATGCTGGCATTC 544
; QY 497 TCAAGAGGTATCAGGGCTTCCTGTTGATGGTCTATGCTGGCATTC 556
; Db 545 TGAACGTCCTCACAAACCAAGTGTCTACACATGCCCTGGTTATCCATTG 604
; QY 557 CTAAGACTTGTGCTGTGAACTGGCTAAGTGTGAA 203
; Db 605 CGAACGCTGGCCAGTCCAGGCCACGTGCTACAGCTCCAGGCTGGTTATCCATTG 636
; QY 322 GTTACACGTGAAACTTCCCCTGTGAGATACCCGCCAGAACCTGAGAGATGGT 381
; Db 336 AGTGCTAGTTGGTCTCCGTTAGAGACCATCCAGTTAGCTCAAAGTCCTC 375
; QY 382 AAGTTAACTTGTGGTCTCTTGATGTTCTAACGCTTGTCAAGCCATGTCAA 441
; Db 376 AACATGGATGATGTTGCGCTTACACACCACTAACATTTACTCTTATTGGAAA 435
; QY 442 GAGGTTTCAAGGGCTCTGTGTTGGT-----TCTATGCTGCTCTGCTATTGG 495
; Db 436 GCTGGTACCAAGAAGATCCTCTAGATGTCCTATGTCCTGCTATTGG 495
; QY 496 ACTAACGATATGGTGTACACATGCCAGGCTGGTGTATCCATTG 555
; Db 556 GCTAAGACTTGTGCTGTGAACTGGCTAAGTCAACATCAGGTTAATTCTTAACCA 615
; Db 556 GCAAGAACTTGTGCTGTCAATTGCCCAAGACATPATCATGTGATTACATGCCCA 615
; QY 616 GTTTACATCTGGCTTACCCAGATATCATGTTAACAGAGAA 666
; Db 616 GGTGTTTCCATCGAAAATGCCCAAGTGGTTGATCGAGTGTGCTGTGAA 666
; RESULT 11
; US-09-367-012-2
; Sequence 2, Application US/09367012
; Patent No. 6218156
; GENERAL INFORMATION:
; APPLICANT: Yashohara, Yoshihiko
; APPLICANT: Kizaki, No. 6218156iyuki
; APPLICANT: Hasegawa, Junzo
; APPLICANT: Wada, Masaru
; APPLICANT: Shimizu, Sakayu
; APPLICANT: Katoka, Michiniko
; APPLICANT: Yamamoto, Kazuhiko
; APPLICANT: Kawabata, Hiroshi
; APPLICANT: Kita, Keiko
; TITLE OF INVENTION: Carbonyl Reductase Enzyme and Methods for its Use
; FILE REFERENCE: 06833.010
; CURRENT APPLICATION NUMBER: US/09/777,157A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/367,012
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Candida magnoliae
; US-09-777-157A-2
; Query Match, Score 51.2; DB 3; Length 852;
; Best Local Similarity 58.6%; Pred. No. 1.2e-05; Gaps 0;
; Matches 89; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
; QY 437 TCAAGAGGTATCAGGGCTTCCTGTTGATGGTCTATGCTGGCATTC 496
; Db 485 TCGAGAGGGCAGAGGGCCCTTGTCACGCCCTCAATGCTGGCATTC 544
; QY 497 TCAAGACTTGTGCTGTGAACTGGCTAAGTGTGAA 203
; Db 545 TGAACGCTGGCCAGTCCAGGCCACGTGCTACAGCTCCAGGCTGGCTGGCCACTTG 604
; QY 557 CTAAGACTTGTGCTGTGAACTGGCTAAGTGTGAA 203

Db 605 CGAAGTCGCTGGCCCTCCTGGATCCAGTGGCGTC 636
; RESULT 13
; Sequence 69, Application US/09734237B
; Patent No. 618752
; GENERAL INFORMATION:
; APPLICANT: Rozzell, J. David
; APPLICANT: Bui, Peter
; TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
; FILE REFERENCE: B593:40008
; CURRENT APPLICATION NUMBER: US/09/734, 237B
; CURRENT FILING DATE: 2000-12-08
; PRIORITY FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Candida magnoliae
; US-09-734-237B-69

Query Match 6.3%; Score 51.2; DB 4; Length 852;
Best Local Similarity 58.6%; Pred. No. 1.2e-05; Matches 89; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 437 TCAAGAGGATCAAGGTCTCTGTGTTGATGGTCTATGCTGGTGCCTTG 496
Db 485 TCGAGAAGGAGCAAGAGGAGGCCCTTGTCACGGCTCAGTGTGCCACATTG 544
Qy 497 TCAACGATCCCTCAAACCAAGATGTTCTACACAGTGTCAAGGCTGGTTATCATTTGG 556
Db 545 TGAACGTCGCCCTGCGGACGTAACCCGGCCAAAGCTGGCGTGCGCACTTCG 604
Qy 557 CTAGACTTTGGCTGTAATGGCTAAGTAC 588
Db 605 CGAAGTCGCTGGCCCTCCTGGATCCAGTGGCGTC 636

RESULT 14
US-09-489-039A-5819
; Sequence 5819, Application US/09489039A
; Patent No. 6160836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PHENOMONAL FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-200401
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5819
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-5819

Query Match 6.3%; Score 51.2; DB 3; Length 1303;
Best Local Similarity 58.6%; Pred. No. 1.5e-05; Matches 89; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 437 TCAAGAGGATCAAGGTCTCTGTGTTGATGGTCTATGCTGGTGCCTTG 496
Db 643 TCGAGAAGGAGGCCAAAGAGGCGCCCTTGTCACGGCCCTCAGTGTGCCACATTG 702
Qy 497 TCAACGATCCCTCAAACGAAAGTGTCTACACATGTCACAGGCTGGTTACATTGG 556
Db 703 TGAACGTCGCCCTGCGGACGTCACGGCCACTAACCGGGCCAGGCTGGCGCCACTTCG 762
Qy 557 CTAGACTTTGGCTGCGTAAGTGGCTAAGGCTGGTCAAGT 588
Db 763 CGAAGTCGCTGGCCCTGCGAGTGTGGCTGGCGTC 794

Search completed: March 2, 2005, 16:57:18
Job time : 195 secs

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On nucleic - nucleic search, using sw model

Run on: March 2, 2005, 04:46:41 ; Search time 560 Seconds
 (without alignments)
 8625.909 Million cell updates/sec

Title: US-10-720-018-1

Perfect score: 816

Sequence: 1 atgactgactacattcaac.....atggtgttcaacttttg 816

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqB, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- 1: _GeneSeq_16Dec04:*
- 2: geneseqn1980s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cb:*
- 11: geneseqn2003db:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	816	100.0	816	Adq94601 Ambroioz
2	99.4	12.2	3203	Aaf07518 Fusarium
3	88.6	10.9	687	Aaf12409 Aspergillus
4	81.8	10.0	637	Adb61049 Bacterial
5	80.6	9.9	735	Adb48561 Bacterial
6	74.6	9.1	852	Aah74598 Synthetic
7	74.2	9.1	1146	Aaf12102 Aspergillus
8	67.6	8.3	783	Adb47380 Bacterial
9	66.4	8.1	789	Adb62512 A. thaliana
10	63.6	7.8	774	Adb41180 Bacterial
11	60.6	7.4	635	Aaf1343 Aspergillus
12	59.8	7.3	822	Aal57425 Datura st
13	59	7.2	774	Aaz46762 Bacteria
14	59	7.2	2255	Aaz46763 Bacillus
15	56.4	6.9	798	Aac42189 Arabidopsis
16	56.4	6.9	825	Aal57426 Hyoscymus
17	56.2	6.9	789	Aac43167 Arabidopsis
18	56.2	6.9	789	Abz1343 Arabidopsis
19	56.2	6.9	789	Adb61514 A. thaliana
20	55.2	6.8	732	Adb63286 Bacterial

ALIGNMENTS

Key	Location/Qualifiers
XX	1. .816
XX	/product= "Ambroiozyma monospora NADH dependent L-xylulose reductase"
XX	/note= "No stop codon"
XX	/EC_number= "EC 1.1.1.10"
XX	US-2004-132074-A1.
XX	08-JUL-2004.
XX	24-NOV-2003; 2003US-00720018.
XX	16-FEB-2001; 2001FI-00003108.
XX	15-FEB-2002; 2002WO-FI000125.
PR	10-MAR-2003; 2003US-00257821.
PR	12-SEP-2003; 2003FI-00013107.
PR	(VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS.
PR	Verho R, Richard P, Penttila M;
XX	WPI; 2004-517001/49.
XX	P-PSDB; ADQ94602.
PT	New DNA molecule encoding NADH dependent L-xylulose reductase, useful in

PT	producing fermentation products or in conversion of cheap biomass to useful products.	RESULT 2	
XX		AAF07518	ID
PS		AAR07518 standard; cDNA; 3203 BP.	XX
CC	The present invention relates to a NADH dependent L-xylose reductase enzyme protein and its encoding polynucleotide. The invention is useful in producing fermentation products or in conversion of cheap biomass to useful products. The present sequence is an Ambrosiozyma monospora NRRL Y-1484 NADH dependent L-xylose reductase cDNA, ALX1 (EC 1.1.1.10).	AC	AAF07518;
CC	-1484 NADH dependent L-xylose reductase cDNA, ALX1 (EC 1.1.1.10).	XX	DT 13-MAR-2001 (first entry)
XX	Sequence 816 BP; 217 A; 159 C; 182 G; 258 T; 0 U; 0 Other;	KW	Fusarium venenatum EST SEQ ID NO:41.
Query Match	100.0%; Score 816; DB 12; Length 816;	KW	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Best Local Similarity	100.0%; Pred. No. 2; e-227;	KW	Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Matches	816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KW	Fusarium venenatum.
Qy	1 ATGAGCTGACTACATTCGAACTTTAGATCGATGGCCACTTACCATATGTCAAGGAGCC 60	OS	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	1 ATGAGCTGACTACATTCGAACTTTAGATCGATGGCCACTTACCATATGTCAAGGAGCC 60	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	61 TGTGGTGGTTAGCTGAGCTTAATCAGGGTTGGCCPACGGTTGCAAGGAGCC 60	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	61 TGTGGTGGTTAGCTGAGCTTAATCAGGGTTGGCCPACGGTTGCAAGGAGCC 60	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	121 TGCCTGATATGACAGAAGAACAGCTGCAAACAGCGAACATACAAATCGCT 180	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	121 TGCCTGATATGACAGAAGAACAGCTGCAAACAGCGAACATACAAATCGCT 180	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	181 ACTGAGAATGGAGTCGAAGAGAGTCGAAGATGGCTTCAAGATGGCTTCAAGTCT 240	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	181 ACTGAGAATGGAGTCGAAGAGAGTCGAAGATGGCTTCAAGTCT 240	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	241 GATTCTGATACCGTTCAAGGGTTGCTCAAGTCTAAGATTTGGTAGTGCCA 300	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	241 GATTCTGATACCGTTCAAGGGTTGCTCAAGTCTAAGATTTGGTAGTGCCA 300	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	301 TTGCACTTGTGTAACAGCTGTTACTGTGAAACTTCCCAGTGAGATTACCGCC 360	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	301 TTGCACTTGTGTAACAGCTGTTACTGTGAAACTTCCCAGTGAGATTACCGCC 360	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	361 AAGAACGCTGAGAGATGCTGAGGTTTACTGTGTTGGCTTCTGAGTTCTCAAGCC 420	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	361 AAGAACGCTGAGAGATGCTGAGGTTTACTGTGTTGGCTTCTGAGTTCTCAAGCC 420	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	421 TTGCTTAAGGCCATTGTCGAAGAGAGTCAAGGGTCTTCTGTTGTTGAGTCT 480	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	421 TTGCTTAAGGCCATTGTCGAAGAGAGTCAAGGGTCTTCTGTTGAGTCT 480	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	481 ATGCTCGTGCCTTCAACGATCTCAAAACCAAGTGTCTACATGCTCAAGCT 540	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	481 ATGCTCGTGCCTTCAACGATCTCAAAACCAAGTGTCTACATGCTCAAGCT 540	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	541 GCTGTTATCCATTGTTAGCTTGTCTGTTGATGGCTTACATCAAGCTCAAGTT 600	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	541 GCTGTTATCCATTGTTAGCTTGTCTGTTGATGGCTTACATCAAGCTCAAGTT 600	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	601 AATTCTTAAACCGAGGTACATCTCGTCTGTTGATGGCTTACATCAAGCTCAAC 660	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	601 AATTCTTAAACCGAGGTACATCTCGTCTGTTGATGGCTTACATCAAGCTCAAC 660	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	661 GAGAATGTTAACCGAGGTACATCTCGTCTGTTGATGGCTTACATCAAGCTCAAC 720	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	661 GAGAATGTTAACCGAGGTACATCTCGTCTGTTGATGGCTTACATCAAGCTCAAC 720	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	721 GATACATTTGGCTGTGTTGACTCTTGTGATCTGCTGCTCATACATCTG 780	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Db	721 GATACATTTGGCTGTGTTGACTCTTGTGATCTGCTGCTCATACATCTG 780	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	781 GCGAGCTTACTGGTTGATGGGTTACTCTCTGG 816	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	781 GCGAGCTTACTGGTTGATGGGTTACTCTCTGG 816	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Qy	308 TGTAAACACCGTGGTACTGTGAAACTCCATGTGAAGATTACCCAGGCAAGACG 367	XX	Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

Db	2614	TAGTCACGTGGCTGCGTCAACGAGAATTGAGGCAATCAACTCCATCGATGTA	2673	XX	
Qy	368	CTGAGAGATGGTGAAAGTTAACCTGTTGGCTTGTGTTCTGAAGCTTGTA	427	CC	The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2674	TSGCAGATGTTGGGGTTTAATGTTGAGCTTACCTTGAGCTTGAGTGC	2733	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	428	AGCCATTGATCAAGAAGGTATCAAGGTGCTCTGTTGTTGATGTTCTATG	487	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2734	A---ACATCTCATGAAGCCAGGTACTTGTTGAGCTTACCTTGAGTGC	2790	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	488	GTCGATGTTCAAGATCTTCAAAACCAGTGTCTAACAGTGTCTAACAGT	547	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2791	GTGCTATGTCAGTCAAGTGTCTAACAGTGTCTAACAGTGTCTAACAG	2850	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	548	TCCATTGCTTAAGACTTGCTGTGTTGAGTGGCTAAGTACAACATCG	607	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2851	GTGCTATGTCAGTCAAGTGTCTAACAGTGTCTAACAGTGTCTAACAG	2910	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	608	TAACCCAGGTACATCTACGGCTCTGAGTGGCTAAGTACAACATCG	667	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2911	TCTCTCTGGCTACATGTTGACTCTAACGGAGATCTGAGATAACCA	2970	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	668	TGACAAACAGATGATCTGTTGATCCACAAAGATGTCGCAACCCAAG	727	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	2971	TGAGAGGAGGACTCTTATCTTCTAGGAGCTACCTGGGACATCTG	3030	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	728	TGCTGCGTTGCTACTGCTTCTGAACTCTGCTCTACACTGTTGCG	787	CC	in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spor morphogenesis, combination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array open reading frames can one gene or open reading frame, and organization of the microarrays based on function of the gene.
Db	3031	TGGTCTCTGTTGCTACT	810	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
Qy	788	TACGGTGTGAGGGGGTCA	3109	CC	products to facilitate analysis of the results. AAF0748 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention
RESULT 3					
AAF12409				XX	
ID	AAF12409	standard; cDNA; 687 BP.		XX	
XX				XX	
AC	AAF12409;			XX	
XX				XX	
DT	13-MAR-2001	(first entry)		XX	
DE	Aspergillus oryzae EST SEQ ID NO:4932.			XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
XX				XX	
OS	Aspergillus oryzae.			XX	
XX				XX	
XX				XX	
PN	W020056762-A2.			XX	
XX				XX	
PD	28-SEP-2000.			XX	
XX				XX	
PP	22-MAR-2000; 2000WO-US007781.			XX	
XX				XX	
PR	22-MAR-1999; 99US1-027363.			XX	
XX				XX	
PA	(NOVO) NOVO NORDISK BIOTECH INC.			XX	
PA	(NOVO) NOVO NORDISK AS.			XX	
XX				XX	
PT	Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;			XX	
XX				XX	
DR	WFI; 2000-594572/56.			XX	
XX				XX	
PT	Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.			XX	
PS	Claim 88; Page 2078; 3161pp; English.			XX	

RESULT	Matches	183; Conservative	0;	Mismatches	147;	Indels	3;	Gaps	1;
4	Qy	304	CACTGGTTACACAGCTGGTACTCGTGAAGATAACCTCCATGTGAGATTAACCCAGCAG	363					
ADS61049	ID	ADS61049	standard; cDNA; 637 BP.						
XX	Db	70	CATCTCTGTCAGTCAGTCAGGGATTACCGAAACATCTGACGCCATCAGTCACCCATACGAC	129					
AC	AC	ADS61049;							
XX	DT	02-DEC-2004	(first entry)						
DE	DE	Bacterial	polymerase #13036.						
XX	KW	Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymerase; gene; ss.							
OS	Bacteria.								
XX	PR	21-FEB-2002; 2002US-0360039P.							
XX	(CAOY/)	CAO Y.							
PA	(HINK/)	HINKLE G J.							
PA	(SLAT/)	SLATER S C.							
PA	(CHEN/)	CHEN X.							
PA	(GOLD/)	GOLDMAN B S.							
XX	PI	Cao Y., Hinkle GJ, Slater SC, Chen X., Goldman BS;							
XX	DR	WPI; 2004-061375/06.							
XX	PT	New recombinant DNA construct comprising a promoter positioned to provide expression of a polymerase encoding a polypeptide from a microbial source, useful for producing plants with improved properties.							
XX	CC	The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymerase encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polymerase or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polymerase used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPRO at seqdata.uspto.gov/sequence.html.							
XX	SQ	Sequence 637 BP; 149 A; 177 C; 169 G; 142 T; 0 U; 0 Other;							
Query Match	PR	10.0%; Score 81.8; DB 13; Length 637;							
Best Local Similarity	PS	55.0%; Pred. No. 3.1e-13;							
CC	CC	The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to							
Match	Qy	364	AACGCTGAGAGATGGTGAAGGTTACTCTGGTTCTGTATGTTCTAACGCCCTTG	423					
Db	Db	130	CGTATGCCAGAGCTCGGGATTACCGAAACATCTGACGCCATCAGTCACCCATACGAC	129					
Qy	Qy	424	GCTAACCCATGATGATCAAAGAGGTTACAGGGTCTCTGTGTTGATGTTGTCATG	483					
Db	Db	190	GCAAGGCACTGAT--GGAGCGAGGCCGGGGAGTTGGCTGATGGTAGCTACGGGRTG	246					
Qy	Qy	484	TCTGGGCACTGTCAGCATGAAACCAAGTGTCTACACATGTCAGTCAGGCTGTTGCT	543					
Db	Db	247	TCTGGGCACTGTCAGCATGTCAGTACCTAACACAAGGCCCTACAAAGCCGCOAGGCC	306					
Qy	Qy	544	GTATCCATTGGCTAGACTTGCTGCTGAATGGCTAAGTACACATCAGGTTAT	603					
Db	Db	307	GTTCGCACCTGTCTGCTTCGGCTGAATGGCAGGACATGGTACAGGTTACAGGTAAC	366					
Qy	Qy	604	TCTTAACCCAGGTACATCTACGGTCTTG	636					
Db	Db	367	TGCATTTGCCGCTGATACAGCTGACTGCTCTG	399					
RESULT	5								
ADS48561	ID	ADS48561	standard; cDNA; 735 BP.						
XX	XX								
AC	ADSA48561;								
XX	XX								
DT	02-DEC-2004	(first entry)							
DE	Bacterial	polymerase #3304.							
XX	KW	Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymerase; gene; ss.							
XX	OS	Bacteria.							
XX	PR	18-DEC-2003.							
XX	US2003233675-A1.								
XX	PP	20-FEB-2003; 2003US-00369493.							
XX	PR	21-FEB-2002; 2002US-0360039P.							
XX	(CAOY/)	CAO Y.							
PA	(HINK/)	HINKLE G J.							
PA	(SLAT/)	SLATER S C.							
PA	(CHEN/)	CHEN X.							
PA	(GOLD/)	GOLDMAN B S.							
XX	PI	Cao Y., Hinkle GJ, Slater SC, Chen X., Goldman BS;							
XX	DR	WPI; 2004-061375/06.							
XX	PT	New recombinant DNA construct comprising a promoter positioned to provide expression of a polymerase encoding a polypeptide from a microbial source, useful for producing plants with improved properties.							
XX	PS	Claim 1; SEQ ID NO 26991; 122pp; English.							
CC	CC	The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to							

provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ sequence 735 BP; 136 A; 234 C; 163 G; 182 T; 0 U; 0 Other;

Query Match 9.9%; **Score** 80.6; **DB** 13; **Length** 735;
Best Local Similarity 61.8%; **Pred No.** 7.4e-13; **Matches** 128; **Conservative** 0; **Mismatches** 79; **Indels** 0; **Gaps** 0;

Qy 436 ATCAGAAGGTTAACGGGTGCTTGTGTTGATGGTCTCATGTCGCGCCATT 495
Db 364 ATGATGGCGCTGGAAACCGGCCATATTCTTGTCGCATGTCGCGCCACATC 423
Qy 496 GTCAAGCTCTCAAAACCAAGTGTCTACACATGTCGCAAGGCGGGTTATCATTG 555
Db 424 GTCACACTACCTCAGGAGGTGCGCTAACGCTCTAAGGCGGGTCATTCAGCTC 483
Qy 556 GCTTAGACTCTGGCTTGATGGCTAAGTACACATCAGGTAATCTTAAACCCA 615
Db 484 GGCAGTCTCTGTGCGCGAGTGGCCAACTACACATCCGGTGTAACTGCAATTCCCC 543
Qy 616 GGTTTACATCTACGGCTTGTGACCG 642
Db 544 GGTACATGGATAACGCCCTGAATAAG 570

RESULT 6

AH74598 standard; DNA; 852 BP.
ID AH74598;
XX
AC
DT 15-OCT-2001 (first entry)

DE Synthetic nucleotide sequence of a NADPH-dependent carbonyl reductase.

KW Methionine gamma lyase; mdeA gene; free folding energy; gene shuffling; directed evolution; molecular breeding; NADPH-dependent carbonyl reductase; ss.

KW Candida magnoliae.

OS PN WO200155342-A2.

XX
PD 02-AUG-2001.

XX
XX
PR 31-JAN-2000; 2000US-00494921.
PR 08-DEC-2000; 2000US-00734237.

PA (BIOC-) BIOCATALYTICS INC.

SQ sequence 852 BP; 196 A; 216 C; 205 G; 235 T; 0 U; 0 Other;

Query Match 9.1%; **Score** 74.6; **DB** 5; **Length** 852;
Best Local Similarity 56.0%; **Pred No.** 4.4e-11; **Matches** 209; **Conservative** 0; **Mismatches** 149; **Indels** 15; **Gaps** 3;

Qy 437 TCAAGAAGGTATCACGGGCTCTCTGTTGATGCTCTCTCTGCGCATG 496
Db 485 TCAAAGAGGATCTAACACCAAGGTGTCACACATGTCACAGCTGGTTGTTGATGCTCTCTGCGCATG 544
Qy 497 TCAACGATCTCAAAACCAAGGTGTCACACATGTCACAGCTGGTTGTTGATGCTCTCTGCGCATG 556
Db 545 TAACTTACCCAGTTCACTACACACAGCTCTAACAGCTGTCATAGCTGTCATGCTCG 604
Qy 557 CTAAAGCTTGCTCTGATGGCTAACGTCACATCAGCTGTTAACCTAACCG 616
Db 605 CTAAATCTCTGGCTGAGAACTGCTCGT---TCCTCGIGTTAACCTGTTCCCG 661
Qy 617 GTTACATCTGGCTCTGGCTGAGAACTGTTAACCTGTTAACCTGTTCCCG 676
Db 662 GCTACATCAAC-----ACCGAAATCTGTACITGGTACCTGGCGAGAACACTCAGAAC 712
Qy 677 GATGGATCTCTGGTATCCACAGAACAAAGATGTCGCAACCAAGGATACTGGTGTG 736
Db 713 ATGGGGTCTCTGGTACCGGGCGTGGGGCAACCTGCTGACTGGTGTGCT 772

Qy 737 TTGGTACTCTCTGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
Db 773 ACCTGTTCTGGCTCTGAA---CGCTGGTCTTACGGCACTGACATCATCGTG 829
Qy 797 ATGGGGTCTGAC 809
Db 830 ACGGGGGTACAC 842

RESULT 7

AAF12302 standard; cDNA; 1146 BP.
ID AAF12302
XX
AC
DT 13-MAR-2001 (first entry)

XX
DB Aspergillus oryzae EST SEQ ID NO:4825.

XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 culture condition; environmental stress; spore morphogenesis;
 metabolic pathway engineering; catabolic pathway engineering; BB.
 KW
 OS Aspergillus oryzae.
 XX
 PN WO20056762-A2.
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US007781.
 XX
 PR 22-MAR-1999; 99US-0027323.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PT Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 substrate of expressed sequence tags.
 PS Claim 88; Page 2039; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential expression of the
 same genes in a first filamentous fungal (FF) cell relative to expression of the
 expression of gene in a second filamentous fungal cells. Monitoring the
 expression of the same genes in one or more second filamentous fungal
 cells. The method uses fluorescence-labeled nucleic acids isolated from
 the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 are used in the methods for monitoring differential expression of gene
 in a first filamentous fungal (FF) cell relative to expression of the
 same genes in one or more second filamentous fungal cells. Monitoring the
 global expression of genes from FF cells allows the production potential
 of the microorganisms to be improved. New genes may be discovered.
 CC possible functions of unknown open reading frames can be identified and
 gene copy number variation and stability can be monitored. The expression
 of genes can be used to study how FF cells adapt to changes in culture
 conditions, environmental stress, sporulation, recombination,
 metabolic or catabolic pathway engineering. Using ESTs provides several
 advantages over genomic or random cDNA clones including elimination of
 redundancy as one spot on an array equals one gene or open reading frame,
 and organisation of the microarrays based on function of the gene
 products to facilitate analysis of the results. AAF07478 to AAF11247
 represents ESTs from Fusarium venenatum; AAF11248 to AAF11653 represents
 ESTs from Aspergillus niger; AAF1854 to AAF14878 represents ESTs from
 Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from
 Trichoderma reesei, which are all specifically claimed in the present
 invention
 XX
 SQ Sequence 1146 BP; 262 A; 313 C; 274 G; 297 T; 0 U; 0 Other;
 Query Match 9.1%; Score 74.2; DB 3; Length 1146;
 Best Local Similarity 50.6%; Pred. No. 6.6e-11; Mismatches 206; Conservative 0; Mismatches 198; Indels 3; Gaps 1;
 Matches 206; Conservative 198; Indels 3; Gaps 1;
 XX
 QY 349 GATTCAGCCAGGAAGCCTGAGATGGAAAGTACTTGTTGGCTCTGTAT 408
 Db 567 GAGTATAGGGCCAGGCCACACCATGTTGCAAGTCAGTCAGTGTCTATG 626
 QY 409 GTTCTCAAGCTTGTAAAGCATTGATGCAAGAAGGTATAAGGGTCTCTGTAT 468
 Db 627 ACTTCCAGGCCGTTGCTAACAAAGTAGTGGCTCGG---CAATGGGGAGCATGCA 683
 QY 469 TTGATTCGTTCTAAGTCCTGGCCATGTCAACGATCTCAAAACCAAGTGTCTAAC 528
 Db 684 CTAACTGGAGCATGAGTGGTCAATGCAATCGGGCTTATCTGCCCTGCTTCAAT 743

QY 529 ATGTCAGGCTGGTCTATCCATTGGCTAAGCTTGGCTGATGGCTAAGTAC 588
 Db 744 GCTAGCAGGCTGAGCTCACTTGCCGTAACCTGCCATGGAATGGGGCGCTAC 803
 QY 589 AACATCAGGTTAATCTTAAACCGGGTACATCTACGCTCTTGACCAAGATGTT 648
 Db 804 AACATCAGGTTAACACATCTGCCGGTACATCTGTTACTGCATGGTGGAGACCTG 863
 QY 649 ATCAATGGTAACGAGATGTCACAGAGATGATCTGTATCCACACAGAGATG 708
 Db 864 TCTGTTGAGTCCCTGCGTGGCTGGAGGAAATGCCAACATAACATGCTGGACGTCTG 923
 QY 709 TCCGAACCAAGGAATCATGGTGTGTTGACTGTGTTCTGA 755
 Db 924 TCTACCCCTAACGAGTACCGTGGCTGGCTCTTCTCTCAGTA 970

RESULT 8
 ID ADS47380 standard; cDNA; 783 BP.
 XX
 AC ADS47380;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polynucleotide #2123.
 XX
 Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 DD 18-DEC-2003.
 XX
 DF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAO Y.) CAO Y.
 PA (HINKL) HINKLE G J.
 PA (SLATE) SLATER S C.
 PA (CHEN X.) CHEN X.
 PA (GOLD) GOLDMAN B S.
 XX
 Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 RS Claim 1; SEQ ID NO 25810; 122pp; English.
 XX
 The invention relates to a recombinant DNA construct comprising a
 promoter functional in a plant cell, where the promoter is positioned to
 provide for expression of a polynucleotide encoding a polypeptide from a
 microbial source. The invention also relates to a transformed plant
 comprising the recombinant DNA construct and a method of producing a
 transformed plant having an improved property. The plant is a crop plant
 such as maize or soybean. The method of producing a transformed plant
 having an improved property comprises transforming a plant with the
 recombinant DNA construct and growing the transformed plant, where the
 polynucleotide or polypeptide is useful for improving plant properties.
 The recombinant DNA construct is useful for producing plants with
 improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulator, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 783 BP; 193 A; 186 C; 173 G; 231 T; 0 U; 0 Other;

Query Match 8.3%; Score 67.6; DB 13; Length 783; Best Local Similarity 51.2%; Pred. No. 4.7e-09; Mismatches 213; Conservative 0; Indels 9; Gaps 2; Matches 213;

Qy 171 CAATAACCTACTGAGAATGAGGTCAAAGAGTGGTCATAGGCTCATATGCCG 230

Db 171 CGAAAGGCTGCAAGGAAATGCGCAGGCTTAATGGTCACACTATACTGCAAGTG 230

Qy 231 TGAATTTCTGATTCGATACCCCTCACAGGGTTCTCAAGTGTCAAGTATTGG 290

Db 231 CGATGCTACTATACCTAAAGAGGTTAACATGCCTTGTGAGATTCAAAGCTTGTGA 290

Qy 291 TAATGCGCATGACTTGTTAACACGGTTACTGGAAGAACTTCCAGTTGCAAGT 350

Db 351 TTACCCAGCCAAAGACGCTGAGAGATGGTAACTTGTGGCTTGTGTATG 410

Qy 348 CATGACTTAGAAGAATGCTATGAATAAACAGTCTCGGTCTCAAGT 407

Db 411 TTTCAAGCCCTTGCTAACGTTACAGTGTCAAGAAGGATTCAGGGTGTCTGTGTT 470

Qy 408 CGTCACATGCTGCCCATCTTCAAAAGCAGG----CCATGGCAGCTTGTAGC 461

Db 471 GATGGTCTATCTGGTCCCATTGTCAAAGCTCTCAAACCAAGTTGTCACACAT 530

Qy 462 TACTGCTTCACTCTGTTAACGGTCCCTAACACAACAGCTGCTAACAC 521

Db 531 GTCCAAGGCTGGTTATGCCATTGGCTAACGTTGCTGTAAGTGGCTAAGT 586

Qy 522 TTCCAAGGCCGGTCACTCACTCATCAAGAGTTGGCAGTCGATGGCCAAAT 577

RESULT 9
ADN62512
ID ADN62512 standard; DNA; 789 BP.

AC ADN62512;
XX DT 01-JUL-2004 (first entry)

DB XX
XX
XX
KW ds; gene; seed size; organ size; plant; transgenic.

XX OS Arabidopsis thaliana.
Key Location/Qualifiers
FH CDS 1..789 /*tag= a
FT CDS
FT
FT KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
XX PN WO2003096797-A2.
XX PD 27-NOV-2003.
XX PP 14-MAY-2003; 2003WO-US014989.
PR XX
OS XX
Bacteria.

XX (MONS) MONSANTO TECHNOLOGY LLC.
PA XX
PI XX
Fernandes M, Xie Z, Dotson SB;
XX DR WI; 2004-042481/04.
DR P-PSDB; ADN62513.

XX PT Increasing seed and organ size of a plant by transforming the plant with a DNA construct comprising a promoter that functions in plants and selecting a desired plant from a population of transformed plants containing the DNA construct.

XX PT Claim 1; SEQ ID NO 17; 71pp; English.

XX CC The invention relates to a novel method for increasing seed and organ size of a plant by: transforming the plant with a DNA construct comprising a promoter that functions in plants, operably linked to a DNA molecule that encodes a protein; and selecting a desired plant from a population of transformed plants containing the DNA construct; where the desired plant exhibits increased seed and organ size compared to a plant of a same plant species not transformed to contain the DNA construct. The method of the present invention is useful for increasing seed and organ size of a plant. The present sequence is used in the exemplification of the invention.

XX SQ Sequence 789 BP; 220 A; 151 C; 183 G; 235 T; 0 U; 0 Other;

XX Query Match 8.1%; Score 66.4; DB 12; Length 789; Best Local Similarity 56.5%; Pred. No. 1.1e-08; Mismatches 165; Conservative 0; Indels 121; Gaps 6; Gaps 2; Matches 165;

Qy 519 TGTCTACAACTGTCAGGCGTGTATCCATTGCTAGACTTGTGCTGATG 578

Db 471 TACTATAGTTAACGAAAGGACTTGTGATCACTGCAAACAACTTGGCATGATG 530

Qy 579 GGCTAAGTACAACTGAGGTTAACTTAAACCCGGTACATCTACGGTCTTGTAC 638

Db 531 GCGAAGGATGCTGATAGGCAACTCTGTTCTCTTAATTTCACCTGCTATGGC 590

Qy 639 CAGAAAGTTATCACTGTAAGGAGTGTACAAACAGATGATCTGTGATATCCACA 698

Db 591 TCAACCTTTTCAAG----AGCCGTTAACGAGAGTTGGTAGACTCCACT 647

Qy 699 ACAAGAATGTCGAMCAANGAAATCATTTGGCTGTTGACTTGCTTCGATC 758

Db 648 TGTCTGCGCTGGAGAGSCAAATGGAG---TTCTACATCTGGCTTTCGTCACC 704

Qy 759 TGTCTCATACACTGGTCCAGCTACTGGTGTATGGTGTTCACT 810

Db 705 TCGAGCTCATATRACTGGTCAGACATTGTTGATGGAGGTCACT 756

RESULT 10
ADS48180
ID ADS48180 standard; cDNA; 774 BP.

AC XX
XX
XX
ADS48180;
XX DT 02-DEC-2004 (first entry)

XX DB Bacterial polynucleotide #2923.

XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
XX OS XX
Bacteria.

PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PP 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINKL/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PT Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 26610; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 774 BP; 226 A; 160 C; 229 G; 159 T; 0 U; 0 Other;
 Query Match 7.8%; Score 63.6; DB 13; Length 774;
 Best Local Similarity 61.4%; Pred. No. 5.9e-08;
 Matches 102; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 472 ATGGGTTCTATGCTGTGCAACATCCTCAAMCAACTGTGTACACATG 531
 Db 436 ATCGGGTCCATGTCGGACACATCGTGAAACACAGCTAACAGCT 495
 QY 532 TCCAAGCTGTGTTATCCATTGCTAGACTTGGCTTGAAATGGCTTAGACAC 591
 Db 496 TCGAAAGGGGGGTGTCATCTACCGAATCTGGCGAGGGGGCCCGTAGGGA 555
 QY 592 ATCAGAGTTAATCTTAATCCAGGTACATCTACGGTCTTGTGA 637
 Db 556 ATCAGGGTGAAGCATAGGCCGGTACATCGAGAACCTCTCA 601
 QY 211 AGATGGTGTATATGCCCTGATATTCTGATTTGACAGGGTCAAGGGTTGCT 270
 Db 200 AAGTCAGCTGCCTATAAGGTGACCTCCGAATCAGGGATATGGAGGTAACTCAG 259
 QY 271 CAAGTGTCTAGGATTGCTAAGTGTGCAATGCACTGTGATCTGAGCTGACTG 330
 Db 260 CAGATGCTCAGCTTGCAGCTTGTGAACTTATGTCGTGAGC--TGGGGTCACT 316
 RESULT 11
 AAF11343
 ID AAF11343 standard; cDNA; 636 BP.
 XX
 AC AAF11343;

QY 331 GAAACTCCATGTGAGATTACCCAGCCAGAACGGCTGAGAGATGGTGAAGGTTAC 390
 CC
 Db 317 TCCNATATGGGGAGAGACTACCCGACATGGCATCATGAGGTCAAT 376
 CC
 QY 391 TGTGCGGTTCTTGATGTTCTCAACGCTTGCTAAGCATGATCAGAGGATTC 450
 CC
 Db 377 CTAGATGGCCATTTATAGGCCAACGGCTTCAGCAGACAGCAGAGGTCAT 432
 CC
 QY 451 AAGGGCTCTGTTGTTGATGGTTATCTGTTGCTGTCAGATCAGACAGCAGG 490
 CC
 Db 433 --ACATGCAAATGAACTCTACAGCCCTGTGAGTCACATGGCAATGCCCTAG 550
 CC
 QY 511 AACCAAGTGTCTCACACATGTCAGGTTGCTAAGACTTGTCT 570
 CC
 Db 491 AAGGAAGTCACATCAACCTCCAAAGCTGGGTGTCGCAATGGCAAATGCTGCT 550
 CC
 QY 571 TGTGAAATGGCTAAGTAC 588
 CC
 Db 551 GTGCAATGGTGGANTTC 568
 CC
 RESULT 12
 AAL57425
 ID AAL57425 standard; DNA; 822 BP.
 XX
 AC AAL57425;
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE Datura stramonium tropinone reductase-1 gene.
 XX
 KW Optically active alcohol; asymmetric ketone reduction; jimsonweed;
 KW tropinone reductase-1; reduced co-enzyme; (R)-3 quinuclidinol;
 KW arteriosclerosis; co-expression; common thornapple; gene; ds.
 XX
 OS Datura stramonium.
 XX
 FH Key Location/Qualifiers
 FT 1. .822
 FT /*tag= a
 FT /product= "Datura stramonium tropinone reductase-1"
 XX
 PN EP1318200-A2.
 XX
 PD 11-JUN-2003.
 XX
 PF 06-DEC-2002; 2002EP-00027311.
 XX
 PR 07-DEC-2001; 2001JP-00375041.
 PR 27-MAY-2002; 2002JP-00152955.
 PR 31-MAY-2002; 2002US-0385434P.
 XX
 PA (DAIL) DAICEL CHEM IND LTD.
 PT Yamamoto H., Ueda M., Ritsuui P., Hamatani T;
 XX
 DR WPI; 2003-51538549.
 DR P-PSDB; AAO27397.
 PT preparation of optically active alcohols, particularly quinuclidinols,
 via asymmetric reduction of a ketone, e.g. 3 quinuclidinone, using
 troponine reductase-I.
 XX
 RS Claim 9; Page 20-21; 30pp; English.

This invention relates to a novel method for the preparation of an optically active alcohol by asymmetric reduction of a ketone with an enzymatic material having tropinone reductase-I activity, in the presence of a reduced co-enzyme. Optically active alcohols are useful in the preparation of optically active compounds, for example (R)-3 quinuclidinol is an intermediate in the preparation of therapeutic agents. These can be used, for example, for the treatment of arteriosclerosis. Co-expression of the 2 enzymes, as in the method of the invention, enables more efficient production of optically active alcohols. The present sequence is the Datura stramonium (jimsonweed; common thornapple) tropinone reductase-1 gene sequence. The protein encoded by this gene was utilised in the method of the invention.

Sequence 822 BP; 255 A; 140 C; 183 G; 244 T; 0 U; 0 Other;
 Query Match 7.3%; Score 59.8; DB 9; length 822;
 Best Local Similarity 52.5%; Pred. No. 9e-07; Mismatches 0; Misnmatches 137; Indels 6; Gaps 1;
 Matches 158; Conservative 0; Db 570
 QY 519 TGCTTACAGATCCAGGCTGCTATCCATTGCTAAGACTTGTCT 578
 CC
 Db 507 TCTTTACTCTAGCTTCCAAAGGGCTAACATAATGACAGATGTTGCGTGTGAC 638
 CC
 QY 579 GCCTTAAGTACAACATGAGTTATTCTTAACCCGGTACATCTACGGTCTTGAC 566
 CC
 Db 567 GGTTAAAGACAGATGGCTGATAGTCCTCCGGAGTCRTTAAACCCACTGT 626
 CC
 Db 639 CAAAAGTATC---AATGGTAAAGAAATCTCTCAAAAGAAATAGACATTATTGCA 692
 CC
 Db 627 TGAAGCTTAAAGAAAATCTCTCAAAAGAAATAGACATTATTGCA 686
 CC
 QY 633 CCCACACAAAGATGGACCAAGGATACATGGTGTGTTGACTTGCTTC 752
 CC
 Db 687 GACTCTPATGGCCGGCGCGGAAAGCCCAAGAGTTCTGCACTAAATAGCTTTCTTG 746
 CC
 QY 753 TGAATCTCTGCCTCATACACTACTGGTGCCAGCTACTGGTGTATGGTTCACTTC 812
 CC
 Db 747 CTTCCTCTCTGCTCATATTCATTCGGCCAGATCATTCGGCTGACCGTTACAGC 806
 CC
 Db 813 T 813
 CC
 Db 807 T 807

RESULT 13
 AAZ46762
 ID AAZ46762 standard; DNA; 774 BP.
 XX
 AC AAZ46762;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Bacillus D-arabinitol dehydrogenase coding sequence.
 XX
 KW D-arabinitol dehydrogenase; clinical diagnosis; mycosis; ds.
 XX
 OS Bacillus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1
 FT /*tag= a
 FT /product= "D-arabinitol dehydrogenase"
 FT /*note= "the stop codon is not indicated"
 XX
 PN JP1132569-A.
 XX
 DD 07-DEC-1999.
 XX
 PP 26-MAY-1998; 98JP-00143637.
 XX
 PR 26-MAY-1998; 98JP-00143637.
 XX
 PA (IKED-) IKEDA SHOKKEN KK.
 PA (NIPK) NIPPON YAKU KK.
 XX
 DR WPI; 2000-091352/08.
 DR P-PSDB; AAV56815.
 XX
 PT Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase - useful as a clinical diagnosing agent for mycosis.
 XX

PT	Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase -
XX	useful as a clinical diagnosing agent for mycosis.
CC	Claim 1; Page 10-11; 14pp; Japanese.
CC	The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from <i>Bacillus</i> sp. IKD 5A868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the coding sequence of the D-arabinitol dehydrogenase.
SQ	Sequence 774 BP; 155 A; 214 C; 271 G; 134 T; 0 U; 0 Other;
Query Match	7.2%; Score 59; DB 3; Length 774;
Best Local Similarity	50.4%; Pred. No. 1.5e-06;
Matches	171; Conservative 0; Mismatches 165; Indels 3; Gaps 1;
QY	478 TCTATGTCMGTGCGCATGGTCAACGATCCTCAAACCAAGTTGTTGCTACACATGCCAG 537
Db	439 TCCATGTCGGGCTATCGTCATAAGCGCGCAGGGCCATACATGTCAG 498
QY	538 GCTGGTGTTATCCATTGCTGCTAACGTTAACCTGCTGATGGCTAACTAACATCAGA 597
Db	499 GCGGGGTGATTTATGCTGACCAAGGTTAACCTGCTGCGTGGCGACGGCTGCAG 558
QY	598 GTTAATCTTAAACCCAGGTTAACCTGCTACGGTCTTCGACCAAGAATTTATCAATGGT 657
Db	559 GTCACACAGTTGCCCGCGCTAGTGAAGAACGAGCTACGGACACCTGATTCGGCCC 618
QY	658 AACGAGAAATGTACACAGATGATCTCTGGTATCCACAACRAAGATGTCGGAACCA 717
Db	619 GGAGGGGAGATGATGACTGACAGTGGTGGATGACCCCGATGGCGCCGGCTCC- 677
QY	718 AACGATACATGGCTGCTGTTGACTCTGTTGAACTGCTGCTTCATACACT 777
Db	678 --GCAGGAGCTGCGGGCATGGCTTACCTGCTCGACGCTTCCTRCGCCAG 735
QY	778 GGAGCCAGCTACTGGTGTGTTGACTCTCTGG 816
Db	736 GGCAGGTTCACTGATGACGGGCTATACGATTGG 774
RESULT 14	AZ246763
ID	AZ246763 standard; DNA; 2255 BP.
XX	AC
XX	AAZ46763;
DT	31-MAR-2000 (first entry)
DB	Bacillus D-arabinitol dehydrogenase encoding genomic DNA.
XX	D-arabinitol dehydrogenase; clinical diagnosis; mycosis; ds.
OS	<i>Bacillus</i> sp.
XX	Key
FH	Location/Qualifiers
FT	*tag= a
FT	/product= "D-arabinitol dehydrogenase"
FT	/note= "the coding sequence is also given in AZ246762"
XX	PN
XX	JP11332569-A.
PD	07-DEC-1999.
XX	
PF	26-MAY-1998; 98JP-00143637.
XX	26-MAY-1998; 98JP-00143637.
PR	
PA	(IKED-) IKEDA SHOKKEN KK.
PA	(NIPK) NIPPON KAYAKU KK.
XX	WPI; 2000-091353/08.
DR	P-PSDB; AAY56815.
RESULT 15	AZC42189
ID	AZC42189 standard; DNA; 798 BP.
XX	AC
XX	AZC42189;
DT	17-OCT-2000 (first entry)
XX	DB
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 34619.
KW	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
KW	OS
XX	Arabidopsis thaliana.
PN	EPI033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000BP-00301439.
XX	
PR	25-FEB-1999; 99US-012185P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-012358P.
PR	23-MAR-1999; 99US-012578P.
PR	25-MAR-1999; 99US-0126268P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127432P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.

PR	16-APR-1999;	99US-0129845P.	PR	19-JUL-1999;	99US-0144334P.
PR	19-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-0144335P.
PR	21-APR-1999;	99US-0130449P.	PR	20-JUL-1999;	99US-0144352P.
PR	23-APR-1999;	99US-0130510P.	PR	20-JUL-1999;	99US-0144652P.
PR	23-APR-1999;	99US-0130891P.	PR	21-JUL-1999;	99US-0144844P.
PR	28-APR-1999;	99US-0131449P.	PR	21-JUL-1999;	99US-0148149P.
PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145068P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	14-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145089P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145089P.
PR	06-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-0145129P.
PR	07-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-0145145P.
PR	11-MAY-1999;	99US-0134226P.	PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	99US-0134218P.	PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-0134219P.	PR	26-JUL-1999;	99US-014526P.
PR	14-MAY-1999;	99US-0134221P.	PR	26-JUL-1999;	99US-014526P.
PR	14-MAY-1999;	99US-0134370P.	PR	27-JUL-1999;	99US-0145913P.
PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145918P.
PR	19-MAY-1999;	99US-0134941P.	PR	27-JUL-1999;	99US-0145919P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146388P.
PR	21-MAY-1999;	99US-0135353P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0145913P.
PR	27-MAY-1999;	99US-0136332P.	PR	27-JUL-1999;	99US-0145919P.
PR	28-MAY-1999;	99US-0136782P.	PR	28-JUL-1999;	99US-0145951P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0146388P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-014760P.
PR	04-JUN-1999;	99US-0137502P.	PR	02-AUG-1999;	99US-0146389P.
PR	07-JUN-1999;	99US-0137724P.	PR	03-AUG-1999;	99US-0145913P.
PR	08-JUN-1999;	99US-0138054P.	PR	04-AUG-1999;	99US-0145919P.
PR	10-JUN-1999;	99US-0138540P.	PR	04-AUG-1999;	99US-0145919P.
PR	10-JUN-1999;	99US-0138847P.	PR	05-AUG-1999;	99US-0146388P.
PR	14-JUN-1999;	99US-0139119P.	PR	05-AUG-1999;	99US-014760P.
PR	16-JUN-1999;	99US-0139452P.	PR	06-AUG-1999;	99US-0146389P.
PR	17-JUN-1999;	99US-0139452P.	PR	06-AUG-1999;	99US-0147244P.
PR	18-JUN-1999;	99US-0139454P.	PR	09-AUG-1999;	99US-0147244P.
PR	18-JUN-1999;	99US-0139455P.	PR	09-AUG-1999;	99US-014735P.
PR	18-JUN-1999;	99US-0139456P.	PR	10-AUG-1999;	99US-014735P.
PR	18-JUN-1999;	99US-0139457P.	PR	11-AUG-1999;	99US-0148319P.
PR	18-JUN-1999;	99US-0139458P.	PR	12-AUG-1999;	99US-0148341P.
PR	18-JUN-1999;	99US-0139459P.	PR	13-AUG-1999;	99US-014855P.
PR	18-JUN-1999;	99US-0139460P.	PR	13-AUG-1999;	99US-0148844P.
PR	18-JUN-1999;	99US-0139461P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139462P.	PR	17-AUG-1999;	99US-0149175P.
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PR	21-JUN-1999;	99US-0139817P.	PR	20-AUG-1999;	99US-0149922P.
PR	22-JUN-1999;	99US-0139899P.	PR	23-AUG-1999;	99US-0149902P.
PR	23-JUN-1999;	99US-0140353P.	PR	23-AUG-1999;	99US-0149930P.
PR	23-JUN-1999;	99US-0140354P.	PR	25-AUG-1999;	99US-0150566P.
PR	23-JUN-1999;	99US-0140354P.	PR	26-AUG-1999;	99US-0150584P.
PR	24-JUN-1999;	99US-0140955P.	PR	27-AUG-1999;	99US-0151065P.
PR	28-JUN-1999;	99US-0140833P.	PR	27-AUG-1999;	99US-0151066P.
PR	29-JUN-1999;	99US-0140931P.	PR	27-AUG-1999;	99US-0151080P.
PR	09-JUN-1999;	99US-0144035P.	PR	30-AUG-1999;	99US-0151303P.
PR	30-JUN-1999;	99US-0144036P.	PR	31-AUG-1999;	99US-01514338P.
PR	01-JUL-1999;	99US-0142920P.	PR	01-SEP-1999;	99US-0151930P.
PR	01-JUL-1999;	99US-0142977P.	PR	07-SEP-1999;	99US-0152363P.
PR	02-JUL-1999;	99US-0142154P.	PR	10-SEP-1999;	99US-0153070P.
PR	06-JUL-1999;	99US-0142055P.	PR	13-SEP-1999;	99US-0153758P.
PR	16-JUL-1999;	99US-0144035P.	PR	15-SEP-1999;	99US-0154018P.
PR	16-JUL-1999;	99US-0144036P.	PR	16-SEP-1999;	99US-0154339P.
PR	12-JUL-1999;	99US-014325P.	PR	20-SEP-1999;	99US-0154779P.
PR	13-JUL-1999;	99US-014325P.	PR	22-SEP-1999;	99US-0155139P.
PR	14-JUL-1999;	99US-0143624P.	PR	23-SEP-1999;	99US-015586P.
PR	15-JUL-1999;	99US-0144005P.	PR	24-SEP-1999;	99US-015586P.
PR	09-JUL-1999;	99US-0142803P.	PR	09-OCT-1999;	99US-0156459P.
PR	16-JUL-1999;	99US-0144035P.	PR	09-OCT-1999;	99US-0156459P.
PR	19-JUL-1999;	99US-014325P.	PR	12-OCT-1999;	99US-0158339P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159339P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.

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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-015984P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160880P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160889P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161932P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 6.9%; Score 56.4; DB 3; Length 798;
Best Local Similarity 54.5%; Pred. No. 8 8e-06; Matches 158; Conservative 0; Mismatches 126; Indels 6; Gaps 2;
Matches 158; Conservative 0; Mismatches 126; Indels 6; Gaps 2;

Qy 521 TCTTACACATGTCAGGGCTGGTGTATCCATTGGCTTAACACTTGGCTGGTGTGAATGG 580
Db 482 TTATAGCTCAACTTAAAGGAGCTTGACCGTTAACGTTAACGGTACATCAGGCTTGGACCA 541
Qy 581 CTAACTACACATCAGGTTAACCTTAACCCAGGTTAACGTTAACGGTACATCAGGCTTGGACCA 640
Db 542 CAAAGAGGGATAAGGCCATGCCTGTGACCTATGTTGTCAGACTCTCTTGCTC 601
Qy 641 AGATGTTATCATGGTACCGAAGAATTTGTCACAGATGGATCTCTGGATCCACAC 700
Db 602 AATTTATCTCGAGG--ACGGGTTCAAGGAGGCTTTCAGTAGAACTCCACTG 658
Qy 701 AAAAGAATGTCACCAACCAAGGAAATACATGGTGGCTGTGTTACTGGCTCTGATCTG 760
Db 659 GTGGCGCTGGAGAGCCGATGAG--TTGCACTAGTGTCTCTCTGGCTTCAACCAG 715
Qy 761 CGGCTTCATACACTCTGGTCCAGCTTACGGTTGATGGGGTTCACT 810
Db 716 CAGCTTCTTATATTACTGGTCAAACCATTTGTTATGGTGGTTCACT 765

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Search completed: March 2, 2005, 14:53:06
 Job time : 564 SECs

ORIGIN	
Query Match	100.0%; Score 816; DB 8; Length 816;
Best Local Similarity	100.0%; Pred. No. 6.3e-196;
Matches	Candidates: 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGACGACTACATGCCAACCTTGTAGTCGATGGCCACTAACATTGTCACAGGCC	60
1 ATGACGACTACATGCCAACCTTGTAGTCGATGGCCACTAACATTGTCACAGGCC	60
61 TCTGGTGTAGCTGAGCTTAATCAGGTTTGCTCAAGATGGCCACTAACATTGTCACAGGCC	60
61 TCTGGTGTAGCTGAGCTTAATCAGGTTTGCTCAAGATGGCCACTAACATTGTCACAGGCC	60
61 TCTGGTGTAGCTGAGCTTAATCAGGTTTGCTCAAGATGGCCACTAACATTGTCACAGGCC	60
181 ACTGAAAGATGAGTGAAGAAGATGCGTCAAAGATGGCTCATGGCTGATGATTTCT	240
181 ACTGAAAGATGAGTGAAGAAGATGCGTCAAAGATGGCTCATGGCTGATGATTTCT	240
241 GATTCGTAACCGTTACAAGGGTGTGCTCAAGTCTAAGGATTTGTTGATGCCA	300
241 GATTCGTAACCGTTACAAGGGTGTGCTCAAGTCTAAGGATTTGTTGATGCCA	300
301 TTGCACTTGGTTAACACAGCTGTTACTGTGAAAGATGGCTCATGGCTGATGATTTCT	240
301 TTGCACTTGGTTAACACAGCTGTTACTGTGAAAGATGGCTCATGGCTGATGATTTCT	240
361 AAGAACCTGAGAGATGGTGGAGCTRACTGTTGGCTTGTGATGTTGATGCC	420
361 AAGAACCTGAGAGATGGTGGAGCTRACTGTTGGCTTGTGATGTTGATGCC	420
421 TTGCACTTGGTTAACACAGCTGTTACTGTGAAAGATGGCTCATGGCTGATGATTTCT	480
421 TTGCACTTGGTTAACACAGCTGTTACTGTGAAAGATGGCTCATGGCTGATGATTTCT	480
481 ATGCTCTGGCCATTGCAACGATCTCCAAACACAGTTGTTACACATGGCTGAGCT	540
481 ATGCTCTGGCCATTGCAACGATCTCCAAACACAGTTGTTACACATGGCTGAGCT	540
541 GCTGTATCCATTGGTAAGACTTGTCTGGTAAAGTCAACTCAAGTT	600
541 GCTGTATCCATTGGTAAGACTTGTCTGGTAAAGTCAACTCAAGTT	600
601 AATTCTTAAACCGGTACATCTACCGTCTTGGCAAGAGATTTATGTAAC	660
601 AATTCTTAAACCGGTACATCTACCGTCTTGGCAAGAGATTTATGTAAC	660
661 GAGAATGTCAGACAGATGGCTCTGGTATCCACACAAAGAATGTCGAAACCAAAG	720
661 GAGAATGTCAGACAGATGGCTCTGGTATCCACACAAAGAATGTCGAAACCAAAG	720
721 GAAATAATTGGCTCTTGTACTCTCTCTGAACTGCGCTCATACACTGGT	780
721 GAAATAATTGGCTCTTGTACTCTCTCTGAACTGCGCTCATACACTGGT	780
781 GCGAGCTACGGTTAGGGGTTACTCTG 816	
781 GCGAGCTACGGTTAGGGGTTACTCTG 816	
RESULT 2	
CTARDH CTARDH 116 bp DNA linear PIN 16-MAY-1995	
LOCUS Candida tropicalis D-arabinitol dehydrogenase (ard) gene, complete cds.	
ACCESSION U00675.1 GI:392785	
KEYWORD	
ORGANISM Candida tropicalis	
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetidae; mitosporic Saccharomycetales; Candida
AUTHORS	1 (bases 1 to 1166)
JOURNAL	Murray,J.S., Wong,M.L., Miyada,C.G., Switchenko,A.C., Goodman,T.C. and Wong,B.
MEDLINE	Gene 155 (1), 123-128 (1995)
PUBMED	95212917
REFERENCE	2 (bases 1 to 1166)
AUTHORS	Wong,B.
JOURNAL	Direct Submission
TITLE	Submitted (10-AUG-1993) Brian Wong, Internal Medicine, University of Cincinnati College of Medicine, 231 Bethesda Avenue, Cincinnati, OH 45267-1560, USA
FEATURES	location/qualifiers
source	1. .1166
gene	/organism="Candida tropicalis"
cds	/mol_type="genomic DNA"
product	/strain="ATCC 750"
protein_id	/db_xref="taxon:5482"
clone	/clone="PCT1A"
functions	/functions="catalyzes D-arabinitol + NAD <=> D-ribulose + NADH"
codon_start	/codon_start=1
evidence_experimental	/evidence=experimental
product	/product="D-arabinitol dehydrogenase"
protein_id	/protein_id="AA66355.1"
db_xref	/db_xref=IGI:92786
translation	/translation="MDSSTSYDNTVPSRDLGKVLINGGSGLSAVUSRALLAKGADIALDMNHLBERTQOARDLQWGEQMKRKHESIPIGOVAWSNGDAEVELIFKAINEHIGKVASVLTNTAGYAPNPAEEYPAKNAENTMKVNGSFVSQAFPLONNMTGSILIGMSGTIVNDPOQWMNSKGAVHSLACEWAKNIRNTSFGYLTPLTRNVISGETMEKTEWESKIPMRMABPEKFVGSILYLAIDSASSYTGHNLWDGYEW"
ORIGIN	
Query Match	40.8%; Score 332.8; DB 8; Length 1166;
Best Local Similarity	65.0%; Pred. No. 1 7e-73;
Matches	Candidates: 528; Conservative 0; Mismatches 272; Indels 12; Gaps 2;
14 TTCCAACTTTGATGGATGCTAACCTAACCTTGTGATCTGATGATGATG	73
278 TTCCAACTTTGATGGATGCTAACCTAACCTTGTGATCTGATGATGATG	337
74 CGAAAGCTTAATCAGGGTTGGCTTAGGTTGACATGCTGATCTGATGATG	133
74 CGAAAGCTTAATCAGGGTTGGCTTAGGTTGACATGCTGATCTGATGATG	133
338 CGCTGTTGTTGCTAACGGCTTGGTCAAGAGTGGCTGATCTGATGATG	397
338 CGCTGTTGTTGCTAACGGCTTGGTCAAGAGTGGCTGATCTGATGATG	397
398 ACTTGGAAAGAACCAACAGCGCAGAGATGTTACATGGGGAAAGACATGA	457
194 ACTTGGAAAGAACCAACAGCGCAGAGATGTTACATGGGGAAAGACATGA	457
458 AAGGAAAGACCAATCTCAATTGGTCAAGTGTGCTGATCTGATGATCTG	517
245 CTCATACGGTTACAGCTGGTTGTGCAAGTGTGCTGATCTGATGATCTG	304
305 ACTGGTTAACACAGCTGGTTGTGCAAGTGTGCTGATCTGATGATCTG	364
578 TTGATTAATCAGCTGGTTGTGCAAGTGTGCTGATCTGATGATCTG	637
365 AGCTGAAAGTGGTCAAGTGTGCTGATCTGATCTGATCTGATCTG	424

Query Match 32.9%; Score 268.4; DB 8; Length 1157;
 Best Local Similarity 60.1%; Pred. No. 3.6e-57;
 Matches 487; Conservative 0; Mismatches 311; Indels 12; Gaps 2;

RESULT 4
CR382133 10/c
WPCOMMENT

Sequence split into 13 fragments LOCUS CR382133 Accession CR382133

Fragment Name	Begin	End
CR382133_00	1	110000
CR382133_01	10001	210000
CR382133_02	20001	310000
CR382133_03	30001	410000
CR382133_04	40001	510000
CR382133_05	50001	610000
CR382133_06	60001	710000
CR382133_07	70001	810000
CR382133_08	80001	910000
CR382133_09	90001	1010000
CR382133_10	100001	1110000
CR382133_11	110001	1210000
CR382133_12	120001	149565

Continuation (11 of 13) of CR382133 from base 100001 (CR382133 Debaromyces hansenii ch

Query Match 33.7%; Score 275.2; DB 8; Length 110000;
 Best Local Similarity 60.6%; Pred. No. 6e-59;
 Matches 492; Conservative 0; Mismatches 308; Indels 12; Gaps 2;

Qy 14 TCCCAACTTTAGATCGATGCCACTAACATTGTCACAGGTGCCTGGTGGTTAG 73
 Db 28160 TCCCAACTTTAGATCGATGCCACTAACATTGTCACAGGTGCCTGGTGGTTAG 28101

Qy 74 CTGAAGCTTAATCAGGTTGTCAGGTCTGACATGCTTGTTGATATCG 133
 Db 28100 CGCTCTGGTGTCTAGCATATTAGCTCGGGAGCACAAATTGCTTGATGA 28041

Qy 134 ACCAAGAAACAACTGTCGCCAACACAGCGATAACACAAATTACGCTACTAGATGA 193
 Db 28040 ATTAGAAAGAACCAAGCGTSCAGCAAGGATTGAAACTGGGACAAAGATCTGA 27981

Qy 194 ACTGAAAGA-----ASPTCCAAAGATGGTTCATAGCTCTGATTTCTGATT 244
 Db 27980 AAGGTGCACATGAAGGCCAAGGGCTGTTCCGATGGCTCTGAAATTGEGGATT 27921

Qy 245 CGATACCGTTACAAGGTTGTCAGGTGCTAAGTGTAGGATTGTAAGTGCATGC 304
 Db 27920 TTAGACAGGTGAAAGTGCTTAAAGACATCAATGACACACAGATATGGGCGATT 27861

Qy 305 ACTGGTTAACACAGCTGTTACTGTGAAACTTCCATGAGATTACCGCCAGA 364
 Db 27860 TCTTAATCAATCTGAGGTACTGTGAGATTCCGGAGATAACATCGCCA 27801

Qy 365 ACCTGTGAAAGATGGTGAAGCTAACGTGTTGGTCTTGTATGTTCTAACGCTTG 424
 Db 27800 ATCTGTGAAAGGTTGGTGAAGCTAACGTGTTGGTCTTGTATGTTCTAACGCTTG 27741

Qy 425 CTAAGCCATTATCAAGAACGATCAAGGSGCTCTGTTGATGTTGTTCTATGT 484
 Db 27740 CGCGTCCATTGATCA--GCACAAATAGAAAGGATCCTACATTTAGTGGTCATGT 27684

Qy 485 CTGGTGCATTCATCAAGATCTCAAAACCCAGTGTGTCAGAACATGTCAGGCGGTG 544
 Db 27683 CTGGAACAACTGTGACGACCCACACACATGTCAGTCAGGCGGTG 27624

RESULT 5

PSARDH
LOCUS PSARDH
DEFINITION P. stipitis ARDH gene encoding D-arabitol dehydrogenase.
ACCESSION Z46866
VERSION Z46866.1
KEYWORDS D-arabitol dehydrogenase.
SOURCE Pichia stipitis
ORGANISM Pichia stipitis
REFERENCE Saecharomycetales; Saccharomycotina; Saccharomycetes;
AUTHORS Baktaryot, Fungi; Ascomycota; Saccharomycetaceae; Pichia.
TITLE 1 (bases 1 to 1157)
JOURNAL Hallborn, J., Walfridsson, M., Penttila, M., Kerranen, S. and
Hahn-Hegerdal, B.
MEDLINE A short-chain dehydrogenase gene from Pichia stipitis having
D-arabitol dehydrogenase activity
PUBMED Yeast 11 (9), 839-847 (1995)
REFERENCE 96090133
AUTHORS Hallborn, J.
TITLE Direct Submission
JOURNAL Submitted (30-Nov-1994) Johan Hallborn, Applied Microbiology, Lund,
 Institute of Technology, Chemical center, Getingeveagen 60, Lund,
 S-221 00, Sweden
FEATURES 7433848
source 2 (bases 1 to 1157)
gene Hallborn, J.
CDS Direct Submission
gene /organism="Pichia stipitis"
mol_type="mRNA"
strain="CBS 6054"
db_xref="taxon:4224"
location 1..1157
qualifiers /db_xref="taxon:4224"
feature Location/Qualifiers
gene /gene="ARDH"
start 191..1027
evidence /evidence="experimental"
product /product="D-arabitol dehydrogenase"
protein_id /protein_id="CAA8939_1"
db_xref /db_xref="GI:763154"
db_xref /db_xref="GO: P50167"
transl /db_xref="UniProt:Swiss-Prot: P50167"
translation /translation="MDSYAYVNPFLRGLIAITGGSGLAIVSRALLAQADVA
 LIDBNLRLKSKAKMEVLGWGEETLKGERASALQVSAMSCNICDAEAVDATFSSINEH
 HKGIAIDLJINTTACYCENPATEYPTAWEISIMVNGGFSYOSPARLPLNLRGS
 ILIGMSGTTVNDPQCMYNNKAGVHPLRQVWAKNIRVWLSPEYLPSVIL
 TRAVISGHMEMKAWESKLPMKRMKAEPKEVSELYLASETASYYTGHNLVWDGVE
CW

		source	1. .696 /organism="unknown" /mol_type="unassigned DNA"
Db	207	CTAAGTGTGTTCCBAACTTCAGATGGAGGAGTTGCCACTTAAACATGGCACAGGTCCTG 64	
Qy	65	GTCGGTTASCTGAAGCTTATCAGGTTGTTGCGCTACGTTGACATGCTTG 124	
Db	267	GTGGTTGGCCCACTCATTCGGTGCCTGTTGGCCAGGGCTGTCCTCA 326	
Qy	125	TGATATGCCAAGAAAGACTGCTGCAAACAGCGATAACACAATACGCTACTG 184	
Db	327	TGACATGAACTTGGAAAGAACCGTCCAAAGAGTTGCGCTGCTGGAG 386	
Qy	185	AAGATGAGTGAAGAGAGTCCAAAGATGGGTCAATG-----CTGTGATA 235	
Db	387	AGACCTTGAGGTGAAACGCTTACAGGTTGTTGCAAGTCACTTCCCTGTC 446	
Qy	236	TTCTGATTCGATTCGGTCAACAGGTTGTTGCTTAAGGTTTGTGTAAGT 295	
Db	447	TTGGGATGTGAGGCAAGCTGAGCTACTTCAAGTGTGTAAGSATTGTAAGT 506	
Qy	296	TGCCNTGGACTTGTAAACACAGCTGTTACTCTGAAACCTCCATGAGATTAC 355	
Db	507	TGCTGACTGTGTTGATTAACACCCTGGTAACCTGAAACTTCCCTCGAAAC 566	
Qy	356	OAGCCAGAAGCTGAGAAGATGGTGAAGGTAACTTGTGTTGGGTTCTG 415	
Db	567	CGACTACTAACGCTGAAAGCATCTGAAAGAGTCAASGGTGTCTGTTGAT 626	
Qy	416	AAGCTTGTCTAAACGATGATCAAGAAGGTATGAGGTTACTCTGTTGATG 475	
Db	627	AATGTTCTGTTAGACGATGATCTGAA---CAACTTGAGGAGCTTACATCTGATG 633	
Qy	476	GTCATGCTGCGCCATGTCAGATCTCAAACCAAGTGTCTAACATGTC 535	
Db	684	GCTCATGTCGGACAACTTGTCAAGGCCAACCCCAATGTATGACATGTC 743	
Qy	536	AGGTGGTGTATCCATTGCTAGACTTGCTAGACTTGGTTGATGGCTAACTACATCA 595	
Db	744	AGGTTGGATGTGATCCACTTGCTAGATCTGGCTGGCATGGCCAGTACACATCA 803	
Qy	596	GAGTTATCTTAAACCCGGTATCATCTACGCTCTTGGCATAGTCAATG 655	
Db	804	GAGTCACACTTAACTACAGGTATATTGTACCTTAACTACAGAAGCTGTTG 863	
Qy	656	GTAAAGAAGATGTACACAGATGATCTCTGTTATCCACAAAGAATGTCGAC 715	
Db	864	GCCACACAGATGAGGAGCCGCTGGAAATCCACCTGAGAGATGCCGAC 923	
Qy	716	CAAAGGAAATCATCTGGCTGTTTGACTCTGCTCTGATCTGCTCTACACTA 775	
Db	924	CCAGGAAATCTGGGGTCATCTATACCTGGCAAGGAGACTCTCTTCACTA 983	
Qy	776	CTGGTGGCCAGCTTACTGGTGTGTTGACTGGTGTGTT 805	
Db	984	CGGCCACHTTGGTTGAGCAGGAGT 1013	
RESULT 6			
AR031556	AR031556	696 bp	DNA
DEFINITION	Sequence 6 from patent US 5866582.		linear
ACCESSION	AR031556		PAT 29-SEP-1999
VERSION	AR031556.1		
KEYWORDS	GI:5945845		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1. (bases 1 to 696)		
AUTHORS	Hallborn,J., Penttila,M., Ojamo,H., Walfridsson,M., Airaksinen,U., Keranen,S. and Hahn-Hagerdal,B.		
TITLE	Xylose utilization by recombinant yeasts		
JOURNAL	Patent: US 586382-A 6 02-FEB-1999;		
FEATURES	Location/Qualifiers		
ORIGIN	/organism="unknown" /mol_type="mRNA"		
Query Match	29.2%	Score 238.2;	DB 6;
Best Local Similarity	64.4%	Pred. No. 17e-49;	
Matches	373;	Conservative 0;	Mismatches 203;
Indels	.	3;	Gaps 1;
Db	227	CCTGTGATTTCTGATCTGATACCGTTCAAGGGTTGCTCAAGTGTAGATT 286	
Db	107	CCTCAACATGGGGATCTGGAGCTAGAGCTACTTTCAGCTCCATCAAGAAC 166	
Qy	287	TGCTAAGTGGCATTSCTGACTTGTGTTACAGCTGCTGCTGCTCCATCA 226	
Db	167	ACGCCAAGATGCGTACTGTGTTGATTTACCGCTGAGTACCTGAGAAC 406	
Qy	347	AAGATACCCAGAAAGACGCTGAGAGATGTTGAGGTTACTCTGTTGGTTCTGT 286	
Db	227	AAAGTACCCGCGCTACTAACGCTGAAAGCATCTGAAGGTGAGCGGTTCCTGC 286	
Qy	407	ATGTTCTGAAAGCTTGTGTTGAACTTCCCTGCGAAACAGTAC 466	
Db	287	ACGTTGGCAATGTTCCCTGACCATGATCGAGA---CAACTTGAGGCT 343	
Qy	467	TGTTGATGGTCTATCTGTTGCTGACATGTTGAGGTTGCTGTTGTTGATG 586	
Db	344	TCTGATGGCTTAATGTCGACATGATCGAGA---CAACTTGAGGCT 526	
Qy	527	ACATGTCGAGGTTGCTTACATTGGCTAGACTTGTGTTGAGTGTGCTA 403	
Db	404	ACATGTCGAGGCTGGACTGTACCTTGCTGAGTGTGCTGAGTGTGCTA 463	
Qy	587	ACAACTGAGGTTAATCTTAAACCCGGTTACATCTACGGCTCTTGCACAGATG 646	
Db	464	ACAACTGAGGCTCAACACTTATCACCGGTATATTGACTCTTAACTACAGA 523	
Qy	647	TATCAAGTGTAGGAGCATCTACAGACAGTGGATCTGTTGATTCACACAAAGA 706	
Db	524	TGTTTCTGCACACAGAGATGAGGAGCTGGGATCCAGATCCCATTGAGAGA 583	
Qy	707	TGTCGAGAACAAAGATACTATGGTGTGTTGACTTGCTTCTGAATGTCCT 766	
Db	584	TGTCGAGAACCCAAAGGAATCTGTTGCTGTTGACTTGCTTCTGAATGTCCT 643	
Qy	767	CATGACTACTGGTGGCTACTGGTGTGATGGTGGTT 805	
Db	644	CCTACACTGGGCCACAGATTGGTGTGGAGGAGAT 682	
RESULT 7			
AR345028	AR345028	696 bp	mRNA
LOCUS	AR345028		linear
DEFINITION	Sequence 6 from patent US 6552944.		PAT 17-AUG-2003
ACCESSION	AR345028		
VERSION	AR345028.1		
KEYWORDS	GI:33741148		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1. (bases 1 to 696)		
AUTHORS	Hallborn,J., Penttila,M., Ojamo,H., Walfridsson,M., Airaksinen,U., Keranen,S. and Hahn-Hagerdal,B.		
TITLE	Production of ethanol from xylose		
JOURNAL	Patent: US 658944-A 6 24-JUN-2003;		
FEATURES	Location/Qualifiers		
source	1. .696 /organism="unknown" /mol_type="mRNA"		
ORIGIN			

Matches	373; Conservative 0; Mismatches 203; Indels 3; Gaps 1;	Db
Qy	227 CCTGTGATATTCTGATTCGTTACCGCTCACAGGTTTCTCAGTCATAAGATT 286	278 CTGGCTGGTATCAAGCTTATTAGCCAAAGGCCGCGATGTCATAGTCGATATGA 337
Db	107 CTCGAACATGGGATCTGAGGAGCTACTTCAGCTCCATCACGACACC 166	134 ACCAAGAACACTGTCGCAAACAGCGAAATCACANATACCTACGAGATGA 193
Qy	287 TTGTAACTTGCCATGCACTTGTACACAGCTGTTACAGCTGAAACTTCCAGT 346	194 AGTGAAGAAAGTCCAA-----AGATGGGTCAATGCCCTGATATTCTGATT 244
Db	167 ACGGCAAGATCGCTGACTGTGATTACACCGCTGATACGTGAAACTTCCCG 226	338 ACTTGAAAGACACAAAGCTGCTGAGAGATGTGAAGGTTACTTGCGGTCTTGT 397
Qy	347 AAAGTACCCAGCCAAGACGCTGAGAGATGTGAAGGTTACTTGCGGTCTTGT 406	245 CTGATACCGTTCACAAAGGTGTTGCTCAAGGAGGTATCAAGGTTCTTCTGTG 304
Db	227 AAAGTACCCAGCCAAGACGCTGAGAGATGTGAAGGTTACTTGCGGTCTTGT 286	458 CTGAAGCTGACTGACATCAAGCCATCAAGGAAACGACACCGCAAATCTGAGT 517
Qy	407 ATGTTCTCAAGCCTTGTCTAACCCATGTCAGAAAGGTATCAAGGTTCTTGTG 466	305 ACTTGTGTCACAGCTGTTACTGAAACTTCCATGTGAGATACCTTGCGATG 364
Db	287 ACCTTCGCATGTTGCTAGACCATGTCAGAA--CAACTGAGACGCTATCA 343	518 TCTTGGCAACACTGCGGTGACGTAATGAACTTCCATTAACAGAAG 577
Qy	467 TTGTGATGGTCTATGCTGGCCATTGTCAGATGGTGGCTCAAAACAGTGTACA 526	365 AGCTGAGAGATGGTGAAGTTACTGTGGTCTTGTGATGTTCTCAAGCTTIG 424
Db	344 TCTGTGATGGCTCATGTCGTGGACAAATGTCACGACCAACATGATGACA 403	578 AGCTGAAACCTTAAGAATGTCACGATCCATTCAGTTCAGTTTG 637
Qy	527 ACATGTCGAAAGCTGGAGTCACTTGTAGATGTTGCTAAGACTTGGTGAATGGCTAAGT 586	425 CTAAAGCATTGATCAAGAAGGTATCAAGGTTCTCAAAACCAAGTGTGTTGTTG 484
Db	404 ACATGTCGAAAGCTGGAGTCACTTGTAGATGTTGCTAAGACTTGGTGAATGGCTAAGT 463	638 CTGACCAATTATCCAAA---CAAGTGAACGGGATGATCATTTGATGGTCAATG 694
Qy	587 ACACATCAGAGTTAATCTTAAACCCAGGTTACATCTACGTCCTTGACCAAGATG 646	485 CTGTCGCATGTCAGATGTCAGGATCTCAAAACCAAGTGTGTTGTTGCTG 544
Db	464 ACACATCAGAGTTAATCTTAAACCCATACCAAGCTATTTGACTCCCTTAACAGAACG 523	695 CGGTACCATGTCAGGACCCACACACACATGATGTCACATGTCACAAACCGGTG 754
Qy	647 TPTCAATGGTAAAGAATGTTACACAAATGAACTCTGTGATGTTCTTGTGATGTTCTCAAGCTTIG 706	545 TTATCCATTGGCTAAAGACTTGGCTTGTGATGGGCTAAGTACACATCAGAGTTATT 604
Db	524 TGATTCTGGCCACAGAGATGAGGAAGGCGGAACTCCATGAGAAAGAA 583	755 TCATCTTGTAGCCAGATCATTTGGCTGTCAATGGCTAAATACATTCAGACTCAACA 814
Qy	707 TGTCCGACCAAGGAAATACATGGCTGTGTTGACTTSCCTTCGAATCTGCTCTT 766	605 CTTAACCCAGGTACACT 625
Db	584 TGGCGAACCAAGGAAATTCTGGGGTCACTTATACTTGGCAAGCAGACTGCTCTT 643	815 CATGGCCCCGGCAACT 835
Qy	767 CTAACTACTGTTGCAAGCTACTGGTTGATGTTGTT 805	RESULT 9 CR382121_09/c
Db	644 CCTPACACTGAGGCCACAAATTGGTGGAGGAGT 682	WPCOMMENT
RESULT 8		
AR54898	AR54898 Sequence 29 from patent US 6747137. DNA linear PAT 08-OCT-2004	Sequence split into 11 fragments Locus CR382121 Accession CR382121
LOCUS	846 bp	Fragment Name Begin End
DEFINITION	DNA	CR382121_00 1 110000
ACCESSION	846 bp	CR382121_01 10001 210000
VERSION	US 6747137.	CR382121_02 20001 310000
KEYWORDS		CR382121_03 30001 410000
SOURCE	Unknown.	CR382121_04 40001 510000
ORGANISM	Unclassified.	CR382121_05 50001 610000
REFERENCE	1. (bases 1 to 846)	CR382121_06 60001 710000
AUTHORS	Weinstock, K.G. and Bush, D.	CR382121_07 70001 810000
TITLE	Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics	CR382121_08 80001 910000
JOURNAL	Patent: US 6747137-A 29 08-JUN-2004;	CR382121_09 90001 101000
FEATURES	source	CR382121_10 100001 1062500
ORIGIN	/organism="unknown"	Continuation[10 of 11] of CR382121 From base 900001 (CR382121 Kluyveromyces lactis stra
Query Match	26.8%; Score 218.6; DB 6; Length 846;	Query Match 19.1%; Score 155.8; DB 8; Length 11000;
Best Local Similarity	62.0%; Pred. No. 1.5e-44; Matches 385; Conservative 0; Mismatches 224; Indels 12; Gaps 2;	Best Local Similarity 53.4%; Pred. No. 1.1e-28; Matches 473; Conservative 0; Mismatches 337; Indels 75; Gaps 4;
Qy	14 TTCCAACTTGTAGTCGATGCCACTAACATTGTCACGGTGCCTGGTGTAG 73	1 ATGACTGACTACATCCAACTTGTAGTCGATGCCACTAACATTGTCACGGTGC 60
Db	218 TCCGAAGCTTGTAGTCGATGAAACTGATTAACCGTGTCTGGTTG 277	61 TTGTGGTGTAGTCGATGCCCTTGTAGTCGATGCCACTAACATTGTCACGGTGT 84150
Qy	74 CTGAAGCTTAAACAGGGTTGGCTACGGTCTGACATGCTTGTGATATCG 133	121 TTGTGGTGTAGTCGACAGAAAGACTGTCGCAACACGGCAATACACAAATACGT 180
Db		84189 TTGTGGTGTAGTCGATGCCCTTGTAGTCGATGAAACTGATTCCTC-- 84133

Continuation (12 of 13) of CR382133 from base 1100001 (CR382133 *Debaromyces hansenii* chro

Query Match 11.3*; Score 92.6; DB 8; Length 110000;
 Best Local Similarity 52.5%; Pred. No. 1.e-12; Matches 309; Conservative 0; Mismatches 259; Indels 21; Gaps 4;

Qy 221 CATA
Db 99071 CTTATAAATGTCCTGTGATAATTTCAGAGAGTAGTAAATGTAATGTGA 280
Qy 281 AGCATTGTTGAGTGCCTACACTGGTTAACAGCTTGTTACTGTGAAACTTC 340
Db 99011 AGGATTGGAACATTGATATTCGTGCTATGCTGGGTTGGGAAATCTGCC 98952
Qy 341 CATGTGAGATTAACCCAGCCAGAACCTGAGAGTGGTAAAGTGTAAAGTGA 400
Db 98951 CAGTAAGCGGAGCTCTCAATGATGCTCCTACACAGTGTGATGAGCGG 98892
Qy 401 CTTGATGTTCTCAAGCCTTGCTAAGCCITGATCAAGAAGGTTACAGGGCTT 460
Db 98891 TTAACTATGC-----AGCCAAATGTTAGGACAAATTGAAAGATGGAAGGAT 98838
Qy 461 CTGTGTTGTTGAGTGGTCTCATGTCCTGGCCATTGTCACAGATCCCAAACAGTTG 520
Db 98837 CATTATAATTACTGCTCCAAAGCTGGACATAGTCACAGTCTTATGCTCAAGTG 98778
Qy 521 TOTACACATGTCACAGCTGCTGTTAACCTGAGTAACTGTTGGCTGTGATGG 580
Db 98777 CCTATAATGCAAGTAAGACGCTCTTACATGCTGGAAATTGCAATTGACTGG 98718
Qy 581 CTAA
Db 98717 TTAGAT---TTCAGAAGTTAACTATATACCAAGCTTAT-----TTGACCG 98670
Qy 641 AGAATGTTATCATGGTAAAGGAAGATGTACACAGATGGAACTCTGGTACACAC 700
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Qy 701 AAAGAATGTCACACCAAGGAAATCATGTTGGCTGTTTACTTGCTTCTGATCTG 760
Db 98609 GGAGAGAGGGTGCACAAAGAATTGACTGGAGCATTTTGTGCACTGAC----G 98553
Qy 761 CGCTCTACATACATCTGGTSCAGCTTACTGGTGTGATGGGGTTAC 809
Db 98552 CATCTACATTCACTACTGGTSCAGCTTAATATCGATGGCGGATATAC 98504

RESULT 12
CR382137_06
WPCOMMENT

Sequence split into 21 fragments LOCUS CR382137 Accession CR382137

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CR382137_02	200002	310000
CR382137_03	300001	410000
CR382137_04	400001	510000
CR382137_05	500001	610000
CR382137_06	600001	710000
CR382137_07	700001	810000
CR382137_08	800001	910000
CR382137_09	900001	1010000
CR382137_10	100001	1110000

RESULT 13

AF002134 AF002134 LOCUS Candida albicans Soup 4293 bp DNA linear PLN 26-JUN-1998 DEFINITION Candida albicans Soup (SOU2), Soup (SOU1) and Vma8p (VMA8) genes, complete cds.

ACCESSION AF002134 VERSION AF002134_1 GI:2103241

KEYWORDS SOURCE Candida albicans

ORGANISM Candida albicans Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic

REFERENCE 1 (bases 1 to 4293)
 AUTHORS Janbon, G., Sherman, F. and Rustchenko, E.
 TITLE Monocopy of a specific chromosome determines L-sorbose utilization:
 a novel regulatory mechanism in *Candida albicans*
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (9), 5150-5155 (1998)
 MEDLINE 98226783
 PUBLISHED 9/5/03
 REFERENCE 2 (bases 1 to 4293)
 AUTHORS Janbon, G., Rustchenko, E. and Sherman, F.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAR-1997) Department of Biochemistry and Biophysics,
 Rochester, NY 14642, USA
 Location/Qualifiers FEATURES source
 1. 4293 /organism="Candida albicans"
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ORIGIN

REFERENCE QY 182 CTGAGAGATGAGGTGTTAAGAGGTCTCAAGATGCGCTCATATGCCGTTGATATTCTG 241
 AUTHORS Db 2286 CTGAAATAATTAACTGAAGAAATGGTCAGGCAAGCTTAAATGTAATGTAAC TG 2345
 TITLE JOURNAL 242 ATCTGATACCGTTCAGAGGTCTCTCAAGTGTCTAAGGATTTGGTAAGTSCAT 301
 MEDLINE 9/5/03
 PUBLISHED 2/14/04
 REFERENCE QY 302 TGCACCTACACGCTGTTACTGTGAAACTCCATGTGAGATPACCIQCCA 361
 AUTHORS Db 2406 TATTTGTTGCTATGCTGGAGTGATGACTGATGAGCAGAACAGGT 2465
 TITLE JOURNAL Submitted (20-MAR-2004) Center for Integrated Fungal Research,
 Rochester, NY 14642, USA
 Location/Qualifiers FEATURES source
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 /note="Vacuolar H+-ATPase subunit 8 homolog"
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RESULT 14 ACI10534/c

DEFINITION AC105434 Magnaporthe grisea chromosome 7 clone 18L14, *** SEQUENCING IN
 PROCESS ***, 2 ordered pieces.

ACCESSION ACI105434

VERSION ACI105434.2 GI:45597494

KEYWORDS HTG; HTGS PHASE2.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea

Bukuryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnorthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 12605)

AUTHORS Thon, M.R., Mitchell, T., Brown, D.E., Diener, S., Taro, A., Pan, H. and Dean, R.A.

TITLE The sequence of Magnaporthe grisea chromosome 7.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12605)

AUTHORS Dean, R.A., Dr. Mitchell, T. Dr., Thon, M. Dr and Brown, D.B.

TITLE Direct Submission

JOURNAL Submitted (05-JAN-2002) Plant Pathology - Fungal Genomics Laboratory, North Carolina State University, 840 Main Campus Drive, Raleigh, NC 27606, USA

REFERENCE 3 (bases 1 to 12605)

AUTHORS Thon, M.R., Mitchell, T., Brown, D.E., Diener, S., Taro, A., Pan, H. and Dean, R.A.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2004) Center for Integrated Fungal Research,

North Carolina State University, Plant Pathology - 840 Main Campus
Dr., Raleigh, NC 27606, USA
On Mar 20, 2004 this sequence version replaced gi:18071329.

* Note: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 86195: contig of 86195 bp in length
86195 86395: gap of unknown length
86395 1.126105: contig of 39710 bp in length.
Location/Qualifiers
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/db_xref="Taxon:148305"
/chromosome="7"
/clone="18114"

ORIGIN

Query Match 10.6%; Score 86.8; DB 2; Length 126105;
Best Local Similarity 53.6%; Pred. No. 3.3e-11;
Matches 328; Conservative 0; Mismatches 279; Indels 24; Gaps 0;
Matches 181; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 464 TGTGTTGATGGTCTATGCTGGGCCATGTCAGACGACTCAACACCGAAGTGTCT 523
Db 56680 TGTCTCTCATCGCAGCTGAGCTGGGGCCATGTCAACGTCGGCAGGGCCCT 56621
Qy 524 ACACATGTCAGGGCTGGTTATCCATTGCTAAAGCTTGCTGTCATGGCTA 583
Db 56620 ACACAGCGTCAAGGCCCGTGGCCACCTGGCCAGCGTGGCCAGTGGGCC 56561
Qy 584 ACTACAACTCGAGTTATCTTAACCGGTTACATTCAGGGTCTTGACCGAGA 643
Db 56560 AGCCGGGATCCGGCTACATGCTCTCCGGCTACATGCTCACCGCCCTGACCAAGA 56501
Qy 644 ATGTTATCAATGGTAAAGGAAGATTGACACAGATGATCTGGTATCCACACAA 703
Db 56500 AGATACHTGAGACAAGGCCGACCTCAAGAGAGAGTGGACAGCAGCTATCCCAGGCA 56441
Qy 704 GAGTGTGGAGACCAAGAAATCATGGTGCTGTTGTTGACTGTCTTCGAAATCTGCTG 763
Db 56440 GATGGGGGCCAGAGGACGCTGATGGCTCCGTCGACTCTGCTGCTGAGCTCG 56381
Qy 764 CTCATGAACTACTGGGCCAESTTACGGTGATGGT 801
Db 56380 TCTAGTGTACCGGGCTGACATCCGTCGATGGCGT 56343

RESULT 15

ARS47359
DEFINITION Sequence 2490 from patent US 6747137.
ACCESSION AR547359
VERSION AR547359.1
KEYWORDS
· SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 927)
AUTORS Weinstock, K.G. and Bush, D.
TITLE Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics
JOURNAL Patent: US 6747137-A 2490 08-JUN-2004;
FEATURES Location/Qualifiers 1. 927
Source /organism="unknown"
/mol_type="genomic DNA."
ORIGIN

Query Match 10.6%; Score 86.6; DB 6; Length 927;
Best Local Similarity 52.0%; Pred. No. 4.3e-11;
Matches 328; Conservative 0; Mismatches 279; Indels 24; Gaps 5;
Matches 181; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

Qy 182 CTGAAGATTAAGTGGAAAGAGTTCACAAAGATGGTCATATGCCGATATTTCTG 241
Db 308 CTGAATATTACCAAGACTTATGGGTTAAATCCAAGGATACAAAGTAAATGTAATG 367
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Db 368 ATTCCAGAGTTGAAAGTGTCAACAAATGACAGTGGATTGGTACCATGATA 427
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Qy 779 GTGCCAACTACTGGTGTGTTGCTTCTGCTGCTTCAACTACTG 809
Db 887 GTGCTGAGCTGTCGTTGATGGTGGTACAC 917

Search completed: March 2, 2005, 15:57:30
Job time : 3861 secs